

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 1, 2002, 12:06:52 ; Search time 25.22 Seconds
(without alignments)
68.594 Million cell updates/sec

Title: US-09-147-490-1
Perfect score: 10
Sequence: 1 LVVYPWQRF 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 17294929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

SPTREMBL.19:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriari:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	10	100.0	17	4	Q9UM85
2	10	100.0	59	4	Q9BXA2
3	10	100.0	61	4	Q14484
4	10	100.0	61	4	Q9UBV6
5	10	100.0	61	4	Q14485
6	10	100.0	89	4	Q9UP81
7	10	100.0	101	4	Q14477
8	10	100.0	101	4	Q14476
9	10	100.0	105	4	Q9BMU5
10	10	100.0	111	4	Q9BWV6
11	10	100.0	113	6	Q02770
12	10	100.0	115	4	Q9G2L9
13	10	100.0	123	4	Q14474
14	10	100.0	125	6	Q28221
15	10	100.0	125	6	Q13072
16	10	100.0	125	6	Q28799

17	10	100.0	128	4	Q9UK54	09UK54 homo sapien
18	10	100.0	129	4	Q9UNL6	09UNL6 homo sapien
19	10	100.0	133	6	Q28552	028552 ovus aries
20	10	100.0	142	6	Q95233	095233 periodicicu
21	10	100.0	142	6	Q13071	013071 callithrix
22	10	100.0	145	6	Q9GJY8	09GJY8 callicebus
23	10	100.0	146	6	Q28460	028460 mirounga an
24	10	100.0	147	4	Q9X96	09X96 homo sapien
25	10	100.0	147	4	Q96FH7	096FH7 homo sapien
26	10	100.0	147	4	Q96FH6	096FH6 homo sapien
27	10	100.0	147	6	Q29415	029415 cebus oliva
28	10	100.0	147	6	Q03901	003901 galago cras
29	10	100.0	147	6	Q03903	003903 macaca mula
30	10	100.0	147	6	Q9GJ57	09GJ57 callithrix
31	10	100.0	147	6	Q9GLX7	09GLX7 salmuri sci
32	10	100.0	147	6	Q9GLX6	09GLX6 salmuri ust
33	10	100.0	147	6	Q9GLX5	09GLX5 actus nancy
34	10	100.0	147	6	Q28779	028779 pan paniscu
35	10	100.0	147	11	Q08752	008752 rattus norv
36	10	100.0	152	4	Q14491	014491 homo sapien
37	10	100.0	155	4	Q14403	014403 homo sapien
38	10	100.0	175	4	Q14473	014473 homo sapien
39	9	90.0	52	6	Q9BEH6	09BEH6 trichosurus
40	9	90.0	52	6	Q9BEH8	061650 mus musculu
41	9	90.0	54	6	Q9BEH9	09BEH9 dasyurus vi
42	9	90.0	58	6	Q9BEH9	09BEH9 macropus gi
43	9	90.0	59	4	Q9BXK3	09BXK3 homo sapien
44	9	90.0	60	6	Q9BEH7	09BEH7 perameles g
45	9	90.0	134	11	Q9CRZ2	09CRZ2 mus musculu
46	9	90.0	146	11	Q9QW91	09QW91 rattus sp.
47	9	90.0	146	11	Q9QUT6	09QUT6 rattus sp.
48	9	90.0	146	11	Q9QUN8	09QUN8 mus musculu
49	9	90.0	146	11	Q9R0S6	09R0S6 mus musculu
50	9	90.0	147	6	Q9BEH1	09BEH1 macropus eu
51	9	90.0	147	6	Q9BEH2	09BEH2 smilthopsis
52	9	90.0	147	11	Q9CY54	09CY54 mus musculu
53	9	90.0	147	11	Q9CY12	09CY12 mus musculu
54	9	90.0	147	11	Q91Y86	091Y86 m 11 days e
55	9	90.0	147	13	Q9YGF5	09YGF5 oncorhynch
56	9	90.0	147	13	Q98UB9	098UB9 notothenia
57	9	90.0	147	13	Q98UB8	098UB8 notothenia
58	9	90.0	163	11	Q9CX22	09CX22 mus musculu
59	8	80.0	15	13	Q90594	090594 gallus gall
60	8	80.0	31	6	Q9BEH0	09BEH0 monodelphis
61	8	80.0	61	11	Q99M06	099M06 cricetus
62	8	80.0	73	11	Q64372	064372 peromyscus
63	8	80.0	73	11	Q62586	062586 peromyscus
64	8	80.0	75	11	Q99M07	099M07 cricetus
65	8	80.0	106	6	Q9XT22	09XT22 ceratotheri
66	8	80.0	106	6	Q9XT22	09XT22 tapirus ter
67	8	80.0	106	6	Q95183	095183 equus cabal
68	8	80.0	125	11	Q9CZG2	09CZG2 mus musculu
69	8	80.0	135	11	Q63066	063066 rattus norv
70	8	80.0	140	11	Q61600	061600 mus musculu
71	8	80.0	146	13	P83133	P83133 diposchels
72	8	80.0	147	11	Q9CZK5	09CZK5 mus musculu
73	8	80.0	147	11	Q98753	098753 rattus norv
74	8	80.0	147	11	Q98754	098754 rattus norv
75	8	80.0	147	11	Q63067	063067 rattus norv
76	8	80.0	147	13	Q90864	090864 gallus gall
77	8	80.0	147	13	Q90938	090938 gallus gall
78	7	70.0	57	4	Q95408	095408 homo sapien
79	7	70.0	69	13	Q9FWM7	09FWM7 morone saxa
80	7	70.0	69	13	Q9FWM5	09FWM5 morone saxa
81	7	70.0	105	13	Q90488	090488 brachydano
82	7	70.0	146	11	Q63011	063011 rattus norv
83	7	70.0	147	11	Q9D0B2	09D0B2 mus musculu
84	7	70.0	147	11	Q9CR49	09CR49 mus musculu
85	7	70.0	147	11	Q62869	062869 rattus norv
86	7	70.0	147	11	Q62670	062670 rattus norv
87	7	70.0	147	13	Q91470	091470 salmo salar
88	7	70.0	147	13	Q9YGF4	09YGF4 oncorhynch
89	7	70.0	147	13	Q9PVL8	09PVL8 hyobius re

90	7	70.0	147	13	Q93548	Q93548	brachydanio
91	7	70.0	147	13	Q91A9	Q91A9	notothenia
92	7	70.0	147	13	Q91471	Q91471	salmo salar
93	7	70.0	147	13	Q91129	Q91129	notothenia
94	7	70.0	147	13	Q90ZM4	Q90ZM4	epinephelus
95	7	70.0	148	13	P70073	P70073	cyprinus ca
96	7	70.0	148	13	Q13140	Q13140	cyprinus ca
97	7	70.0	148	13	Q98851	Q98851	cyprinus ca
98	7	70.0	148	13	Q98852	Q98852	cyprinus ca
99	7	70.0	148	13	Q98853	Q98853	cyprinus ca
100	7	70.0	148	13	Q90485	Q90485	brachydanio

ALIGNMENTS

RESULT	1			
Q9UM85				
ID	Q9UM85	PRELIMINARY;	PTT;	17 AA.
AC	Q9UM85;			
DT	01-MAY-2000	(TREMBLrel. 13, Created)		
DT	01-MAY-2000	(TREMBLrel. 13, last sequence update)		
DT	01-DEC-2001	(TREMBLrel. 13, last annotation update)		
DE	BETA-GLOBIN PROTEIN (FRAGMENT).			
GN	BETA-GLOBIN.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxId:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=66352914; PubMed=8718696;			
RA	Rahbar S., Nozari G., Forrest G., Gelbart T., Forman S.J., Beutler E.			
RT	"A novel intrachromosomal rearrangement in the beta-globin gene found			
RL	in an African-American family.";			
EMBL	Hemoglobin 19:375-388(1995).			
DR	EMBL: S83767; AAD14420.1; .			
DR	HSSP: P02023; 1ABW.			
FT	NO_TERM	1	1	
SQ	SEQUENCE	17 AA;	2104 MW;	4197755B5260504 CRC64;

Query Match	100.0%;	Score 10;	DB 4;	Length 17;
Best Local Similarity	100.0%;	Pred. No. 1.2e-05;		
Matches 10;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	LVVYPTQRF	10
Db	2	LVVYPTQRF	11

RESULT	2		
09BXA2			
ID	09BXA2	PRELIMINARY;	PT; 59 AA.
AC	09BXA2;		
DT	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2001 (TREMBLrel. 17, last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, last annotation update)		
DE	BETA-GLOBIN (FRAGMENT).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxId:9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Kutluer F., Agulnaga P.M., Glendenning M., Kutluer A.;		
RT	"IVS-1-5 G to C Homozygous Beta Thalassemia Mutation was Detected in a		
RT	Kurdish Patient.";		
RL	Submitted (FEB-2001) to the EMBL/Genbank/DBJ		
CC	- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.		
DR	EMBL: AF348448; AAK30154.1; -.		
DR	HSSP: P02023; 1DXT		
DR	Interpro: IPR002337; Beta_hem.		

DR InterPro: IPR0000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PS00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport; Respiratory protein
FT NON_TER 59
SQ SEQUENCE 59 AA; 6463 MW; 128BE2C12A13A9D3 CRC64;

Query Match	100.0%;	Score 10;	DB 4;	Length 59;
Best Local Similarity	100.0%;	Pred. No. 3.2e-05;		
Matches 10;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	LVVYPTQRF	10
Db	33	LVVYPTQRF	42

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RESULT 3
014484 ID 014484 PRELIMINARY; PRT; 61 AA.
AC 014484;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-CC-2001 (TReMBLrel. 18, Last annotation update)
DE BETA-HEMOGLOBIN (FRAGMENT).
GN HBB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE-87299720; PubMed-3620470;
RA Liu J.Z., Harano T., Lanclos K.D., Huisman T.H.;
RT "The beta-delta crossover leading to the beta delta hybrid gene of
RT hemicoglobin P-NiIotic is located within 54 base-pairs of the 5' end of
RT exon 2 or between codons 31 and 50."
RL Biochim. Biophys. Acta 909:208-212(1987).
[2]
RP SEQUENCE FROM N.A.
RA Fullerton S.M., Bond J., Schneider J.A., Hamilton B., Harding R.M.,
RA Boyce A.J., Clegg J.B.;
RT "Polymorphism and divergence in the beta-globin replication origin
RT initiation region."
RL Mol. Biol. Evol. 0:0-0(1999).
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL: M25660; AAA53153.1; -
DR EMBL: AF186620; AAF08272.1; -
DR EMBL: AF186606; AAF08258.1; -
DR EMBL: AF186608; AAF08260.1; -
DR EMBL: AF186609; AAF08261.1; -
DR EMBL: AF186610; AAF08262.1; -
DR EMBL: AF186611; AAF08263.1; -
DR EMBL: AF186612; AAF08264.1; -
DR EMBL: AF186613; AAF08265.1; -
DR EMBL: AF186615; AAF08267.1; -
DR EMBL: AF186616; AAF08268.1; -
DR EMBL: AF186617; AAF08269.1; -
DR EMBL: AF186618; AAF08270.1; -
DR EMBL: AF186619; AAF08271.1; -
DR HSSE; P02023; IDXT.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Respiratory protein.
FT NON_TER 61
SQ SEQUENCE 61 AA; 6691 MW; 905E928EF2C12A13 CRC64;
Query Match 100.0%; Score 10; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 LVVYPWTFORF 10
 |||||||||
 DB 33 LVVYPWTFORF 42

RESULT 4

OYUBV6 PRELIMINARY; PRT; 61 AA.
 AC OYUBV6;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)

DE BETA-GLOBIN (FRAGMENT).

GN HBB.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Fullerton S.M., Bond J., Schneider J.A., Hamilton B., Harding R.M.,

Boyce A.J., Clegg J.B.;

RT "Polymorphism and divergence in the beta-globin replication origin

initiation region."

RL Mol. Biol. Evol. 0:0-0(1999).

CC -1. SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

DR EMBL; AF186614; AAF08266.1; -.

DR HSSP; P02023; 1HBS.

DR InterPro: IPR002337; Beta.haem.

DR InterPro: IPR000971; Globin.

DR Pfam; PF00042; globin; 1.

DR PRINTS; PR00814; BETAHAEM.

DR PROSITE; PS01033; GLOBIN; 1.

KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.

FT NON_TER 61

SEQUENCE 61 AA: 6661 MW; 304D818EF2C13455 CRC64;

Query Match 100.0%; Score 10; DB 4; Length 61;

Best Local Similarity 100.0%; Pred. No. 3.3e-05;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFORF 10
 |||||||||
 DB 33 LVVYPWTFORF 42

RESULT 5

OYUBV6 PRELIMINARY; PRT; 61 AA.
 AC OYUBV6;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)

DE DELTA-HEMOGLOBIN (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Liu J.Z., Harano T., Lanclos K.D., Huisman T.H.;

RT "The beta-delta crossover leading to the beta delta hybrid gene of

DR Pfam; PF00042; globin; 1.
 DR PROSITE; PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Respiratory protein.
 FT NON_TER 61
 SQ SEQUENCE 61 AA: 6661 MW; D5DC4F2CC2DDF822 CRC64;

Query Match 100.0%; Score 10; DB 4; Length 61;

Best Local Similarity 100.0%; Pred. No. 3.3e-05;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFORF 10
 |||||||||
 DB 33 LVVYPWTFORF 42

RESULT 6

OYUBV6 PRELIMINARY; PRT; 89 AA.
 AC OYUBV6;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)

DE MUTANT BETA-GLOBIN.

GN HBB.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Cabeda J.M., Correia C., Estevinho A., Cardoso C., Amorim M.L.,

Cleto E., Vale L., Coimbra E., Pinho L., Justica B.;

RT "Unexpected pattern of beta-globin mutations in beta-thalassemia

patients from northern Portugal."

RL Br. J. Haematol. 105:68-74(1999).

CC -1. SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

DR EMBL; AF059180; AAD30656.1; -.

DR HSSP; P02070; 1HDA.

DR InterPro: IPR002337; Beta.haem.

DR InterPro: IPR000971; Globin.

DR Pfam; PF00042; globin; 1.

DR PRINTS; PR00814; BETAHAEM.

DR PROSITE; PS01033; GLOBIN; 1.

KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.

FT NON_TER 89

SEQUENCE 89 AA: 9689 MW; 4A138B28BEEF0D1 CRC64;

OY 1 LVVYPWTFORF 10
 |||||||||
 DB 33 LVVYPWTFORF 42

Query Match 100.0%; Score 10; DB 4; Length 89;

Best Local Similarity 100.0%; Pred. No. 4.5e-05;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFORF 10
 |||||||||
 DB 33 LVVYPWTFORF 42

RESULT 7

OYUBV6 PRELIMINARY; PRT; 101 AA.
 AC OYUBV6;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)

DE HBB PROTEIN (FRAGMENT).

GN HBB.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-84178511; Pubmed-6324786;
RA Kimura A., Ohta Y., Fukumaki Y., Takagi Y.;
RT "A fusion gene in man: DNA sequence analysis of the abnormal globin
RT gene of hemoglobin Miyada.";
RL Biochem. Biophys. Res. Commun. 119:968-974(1984).
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL; K01899; AAA52635.1; -.
DR HSSP; P02023; IDXT.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR InterPro: IPR002335; Myoglobin.
DR Pfam: PF00042; globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PRINTS; PR00613; MYOGLOBIN.
DR PROSITE; PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
FT NON_TER 101
SQ SEQUENCE 101 AA; 10928 MW; F54BFD8224B5DB0F CRC64;

Query Match 100.0%; Score 10; DB 4; Length 101;
Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTORF 10
| | | | | | | | | |
DB 33 LVVYPTORF 42

RESULT 8
ID Q14476 PRELIMINARY; PRT; 101 AA.
AC Q14476;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE G-GAMMA-HEMOGLOBIN GENE FROM GREEK HPEH MUTANT (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE-86017015; Pubmed-2413469;
RA Gellinas R., Yagci M., Endlich B., Lotshaw C., Kazazian H.H.Jr. .;
RA Stamatoyanopoulos G.;
RT "Sequences of G-gamma, A-gamma, and beta genes of the Greek (A-gamma)
RT HPEH mutant: evidence for a distal CCAAT box mutation in the A-gamma
RT gene.";
RL Prog. Clin. Biol. Res. 191:125-139(1985).
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL; M32723; AAA35955.1; -.
DR HSSP; P02096; IFDH.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR InterPro: IPR002335; Myoglobin.
DR Pfam: PF00042; globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PRINTS; PR00613; MYOGLOBIN.
DR PROSITE; PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
FT NON_TER 101
SQ SEQUENCE 101 AA; 11039 MW; 8489D25BBD829BA5 CRC64;

Query Match 100.0%; Score 10; DB 4; Length 101;
Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTORF 10
| | | | | | | | | |
DB 33 LVVYPTORF 42

RESULT 9
ID Q9BWU5 PRELIMINARY; PRT; 105 AA.
AC Q9BWU5;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MUTANT HEMOGLOBIN BETA CHAIN (FRAGMENT).
GN HBB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE-BLOOD;
RA Kular F., Leitner C., Briscoe J., Kular A.;
RT "Hemoglobin S (Glu 6 Val) +D-Ibadan (Thr 87 Lys): two beta chain
RT variants were detected in an African-American individual by sequencing
RT of the beta globin gene.";
RL Submitted (FE8-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL; AY027800; AK15811.1; -.
DR HSSP; P02023; ZHBS.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
FT VARIANT 7 88 V -> E.
FT VARIANT 8 88 K -> T.
FT NON_TER 105
SQ SEQUENCE 105 AA; 11501 MW; 8143C84D90C01687 CRC64;

Query Match 100.0%; Score 10; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 5.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTORF 10
| | | | | | | | | |
DB 33 LVVYPTORF 42

RESULT 10
ID Q9BWV6 PRELIMINARY; PRT; 111 AA.
AC Q9BWV6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MUTANT BETA GLOBIN.
GN HBB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE-BLOOD;
RA Kular F., Adekunle A.D., Leitner C., Kular A.;
RT "Double heterozygous beta thalassemia mutation (promoter region - 28 A
RT to C; IVS-II-1 region G to A) was found in a Kuwaiti patient.";
RL Submitted (FE8-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL; AY027509; AAK20080.1; -.
DR HSSP; P02023; IDXT.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PRINTS; PR00814; BETAHAEM.

DR PROSITE; PS01033; GLOBIN; 1.
 KM Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 FT VARIANT 106 106 M -> V
 SQ SEQUENCE 111 AA; 12234 MW; 8992F924B5B3903A CRC64;

Query Match 100.0%; Score 10; DB 4; Length 111;
 Best Local Similarity 100.0%; Pred. No. 5.5e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
 |||||
 DB 33 LVVYPWTQRF 42

RESULT 11
 002770 PRELIMINARY; PRT; 113 AA.

AC 002770;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE EPSILON-GLOBIN (FRAGMENT).
 OS Callithrix argentata (Black-tailed marmoset).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
 OX NCBI_TaxID=9482;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98121278; PubMed=9461380;
 RA Porter C.A., Czelusniak J., Schneider H., Schneider M.P., Sampaio I.,
 RA Goodman M.A.;

"Sequences of the primate epsilon-globin gene: implications for
 RT systematics of the marmosets and other New World primates.";
 RL Gene 205:59-71(1997).
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: U97025; AAC39571.1; -.
 DR HSSP: P02100; 1A9W.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR InterPro: IPR002335; Myoglobin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PRINTS: PR00613; MYOGLOBIN.
 DR PROSITE: PS01033; GLOBIN; 1.
 DR Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 FT NON_TER 113 113
 SQ SEQUENCE 113 AA; 12499 MW; 994B7D3BEC81D9D CRC64;

Query Match 100.0%; Score 10; DB 6; Length 113;
 Best Local Similarity 100.0%; Pred. No. 5.5e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
 |||||
 DB 33 LVVYPWTQRF 42

RESULT 12
 09GZL9 PRELIMINARY; PRT; 115 AA.

AC 09GZL9;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE BETA-GLOBIN (MUTANT BETA-GLOBIN) (FRAGMENT).
 GN HBB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Yang Z., Chu J., Ban G., Shi L., Huang X., Lin K., Tao Y.,
 RT "Molecular characterization of beta thalassemia in Yunnan, China."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: AY013302; AAG46185.1; -.
 DR EMBL: AY013301; AAG46184.1; -.
 DR HSSP: P02023; 1DXT.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 DR Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 FT NON_TER 115 115
 SQ SEQUENCE 115 AA; 12528 MW; FA179881D9CAB81B CRC64;

Query Match 100.0%; Score 10; DB 4; Length 115;
 Best Local Similarity 100.0%; Pred. No. 5.6e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
 |||||
 DB 33 LVVYPWTQRF 42

RESULT 13
 014474 PRELIMINARY; PRT; 123 AA.

AC 014474;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE A-GAMMA-HENOGLOBIN GENE FROM GREEK HPFH MUTANT (FRAGMENT).
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86017015; PubMed=2413469;
 RA Gellinas R., Yagi M., Endlich B., Lotshaw C., Kazazian H.H.Jr. ,
 RA Stamatoyanopoulos G.;
 RT "Sequences of G-gamma, A-gamma, and beta genes of the Greek (A-gamma)
 RT HPFH mutant: evidence for a distal CCAAT box mutation in the A-gamma
 RT gene.";
 RL Proc. Clin. Biol. Res. 191:125-139(1985).
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: M32724; AAA35953.1; -.
 DR HSSP: P02096; 1FDH.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR InterPro: IPR002335; Myoglobin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PRINTS: PR00613; MYOGLOBIN.
 DR PROSITE: PS01033; GLOBIN; 1.
 DR Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 FT NON_TER 123 123
 SQ SEQUENCE 123 AA; 13510 MW; 7C42739B2FA2FC1 CRC64;

Query Match 100.0%; Score 10; DB 4; Length 123;
 Best Local Similarity 100.0%; Pred. No. 5.9e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
 |||||
 DB 33 LVVYPWTQRF 42

RESULT 14

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028221 ID 028221 PRELIMINARY: PRT: 125 AA.
AC 028221:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GAMMA-1 GLOBIN.
GN GAMMA-1 GLOBIN.
OS Cebus albifrons (White-fronted capuchin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Cebus.
NCBI_TaxID=9514;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=94102757; PubMed=8276414;
RA Hayasaka K., Skinner C.G., Goodman M., Slightom J.L.;
RT "The gamma-globin genes and their flanking sequences in primates:
RT findings with nucleotide sequences of capuchin monkey and tarsier.";
RL Genomics 18:20-28(1993).
RN 12
RP SEQUENCE FROM N.A.
RX MEDLINE=94115696; PubMed=1342932;
RA Bailey W.J., Hayasaka K., Skinner C.G., Kehoe S., Sieu L.C.,
RA Slightom J.L., Goodman M.;
RT "Reexamination of the African hominoid trichotomy with additional
RT sequences from the primate beta-globin gene cluster.";
RL Mol. Phylogenet. Evol. 1:97-135(1992).
RN 13
RP SEQUENCE FROM N.A.
RA Hayasaka K., Skinner C.G., Slightom J.L., Goodman M.;
RT "Molecular phylogeny of three platyrrhine primates, capuchin monkey,
RT spider monkey, and owl monkey, as inferred from nucleotide sequences
RT of the pseudo-eta-globin gene.";
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL: M81409; AAA19703.1; -.
DR HSSP: P02096; IFDH.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PROSITE: PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Respiratory protein.
SQ SEQUENCE 125 AA; 13534 MW; ADIC8A32D49179BF CRC64;

Query Match 100.0%; Score 10; DB 6; Length 125;
Best Local Similarity 100.0%; Pred. No. 6e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10
DB 33 LVVYPTQRF 42

RESULT 15
O13072 ID 013072 PRELIMINARY: PRT: 125 AA.
AC 013072:
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE EPSILON-GLOBIN (FRAGMENT).
OS Callithrix jacchus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callitrich.
NCBI_TaxID=57377;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=98121278; PubMed=9461380;
RA Porter C.A., Czelusniak J., Schneider H., Schneider M.P., Sampalo I.,
RA Goodman M.;
RT "Sequences of the primate epsilon-globin gene: implications for
RT systematics of the marmosets and other New World primates.";
RL Gene 205:59-71(1997).

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CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL: U97024; AAC39570.1; -.
DR HSSP: P02100; IAGM.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR InterPro: IPR002335; Myoglobin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00814; BETAHAEM.
DR PRINTS: PR00613; MYOGLOBIN.
DR PROSITE: PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
FT NON_TER 125
SQ SEQUENCE 125 AA; 13842 MW; D31A007C586B6C7C CRC64;

Query Match 100.0%; Score 10; DB 6; Length 125;
Best Local Similarity 100.0%; Pred. No. 6e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10
DB 33 LVVYPTQRF 42

RESULT 16
O28799 ID 028799 PRELIMINARY: PRT: 125 AA.
AC 028799:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BETA-GLOBIN (FRAGMENT).
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
NCBI_TaxID=9598;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=85210896; PubMed=399143;
RA Savatier P., Tribuchet G., Faure C., Chebloune Y., Gouy M.,
RA Verdier G., Nigon V.M.;
RT "High Rate of Variation in CpG Dinucleotides and in Short Repeated
RT Sequences between Man and Chimpanzee.";
RL J. Mol. Biol. 182:21-29(1985).
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL: X02345; CAA26204.1; -.
DR HSSP: P02023; IDXT.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
FT NON_TER 125
SQ SEQUENCE 125 AA; 13662 MW; 6790E535F7A11230 CRC64;

Query Match 100.0%; Score 10; DB 6; Length 125;
Best Local Similarity 100.0%; Pred. No. 6e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10
DB 37 LVVYPTQRF 46

RESULT 17
O9UK54 ID 09UK54 PRELIMINARY: PRT: 128 AA.
AC 09UK54:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

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DE HEMOGLOBIN BETA SUBUNIT VARIANT (FRAGMENT).
 GN HBB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BLOOD;
 RA Kutlar F., Holley L., Leitner C., Brisco J., Kutlar A.;
 RT "A silent, very unstable, thalassemic hemoglobin variant, detected by
 RT cDNA sequencing of beta globin mRNA (hemoglobin Hradec Kralove) found
 RT in an African American Baby";
 RL Submitted (MUG-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: AF181832; AF00488.1; -.
 DR HSSP: P02023; IBAH.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR InterPro: IPR002335; Myoglobin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PRINTS: PR00613; MYOGLOBIN.
 DR PROSITE: PS01033; GLOBIN; 1.
 KM Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 FT NON_TER 1
 FT VARIANT 97 97 D -> A
 SQ SEQUENCE 128 AA; 13964 MW; 398888E71EBE48A2 CRC64;
 Query Match 100.0%; Score 10; DB 4; Length 128;
 Best Local Similarity 100.0%; Pred. No. 6.1e-05; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVVYPWTQRF 10
 |||||
 DB 14 LVVYPWTQRF 23
 RESULT 18
 Q9UNL6 PRELIMINARY; PRT; 129 AA.
 AC Q9UNL6;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE HEMOGLOBIN GAMMA-G (FRAGMENT).
 GN HBG2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BLOOD;
 RA Kutlar F., Prchal J.T., Leitner C., Kutlar A.;
 RT "Nucleotide sequence of the human G-gamma globin messenger RNA
 RT isolated from whole blood.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: AF104493; A019655.1; -.
 DR HSSP: P02096; IPDH.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR InterPro: IPR002335; Myoglobin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PRINTS: PR00613; MYOGLOBIN.
 DR PROSITE: PS01033; GLOBIN; 1.
 KM Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 FT NON_TER 1
 FT SEQUENCE 129 AA; 14093 MW; 605C30E6FA3B20A4 CRC64;

Query Match 100.0%; Score 10; DB 4; Length 129;
 Best Local Similarity 100.0%; Pred. No. 6.2e-05; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVVYPWTQRF 10
 |||||
 DB 15 LVVYPWTQRF 24
 RESULT 19
 Q28552 PRELIMINARY; PRT; 133 AA.
 ID Q28552;
 AC Q28552;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE FETAL GLOBIN.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94250699; PubMed=8193169;
 RA Saban J., King D.;
 RT "Sequence of the sheep fetal beta globin gene and flanking region.";
 RL Biochim. Biophys. Acta 1218:87-90(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8117290; PubMed=6161931;
 RA Kretschmer P.J., Coon H.C., Davis A., Harrison M., Nienhuis A.W.;
 RT "Hemoglobin switching in sheep: Isolation of the fetal gamma-globin
 RT gene and demonstration that the fetal gamma- and adult beta-A-globin
 RT genes lie within eight kilobase segment of homologous DNA.";
 RL J. Biol. Chem. 256:1975-1982(1981).
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: U01378; A019218.1; -.
 DR HSSP: P02070; IHAH.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KM Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 SQ SEQUENCE 133 AA; 14780 MW; C0E3736E79BF93C CRC64;
 Query Match 100.0%; Score 10; DB 6; Length 133;
 Best Local Similarity 100.0%; Pred. No. 6.3e-05; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVVYPWTQRF 10
 |||||
 DB 19 LVVYPWTQRF 28
 RESULT 20.
 Q95233 PRELIMINARY; PRT; 142 AA.
 ID Q95233;
 AC Q95233;
 DT 01-FEB-1997 (TREMblrel. 02, Created)
 DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE EPSILON GLOBIN (FRAGMENT).
 OS Perodicticus potto (Potto).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Strepsirrhini; Loridae; Perodicticus.
 OX NCBI_TaxID=9472;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Porter C.A., Page S.L., Czelusniak J., Schneider H., Schneider M.P.C.,

RA Sampalo I., Goodman M.;
 RT "Phylogeny and evolution of selected primates as determined by
 sequences of the epsilon-globin locus and 5' flanking regions."
 RL Int. J. Primatol. 18:261-295(1997).
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: U64617; AAB60784.1; -.
 DR HSSP: P02100; 1A9W.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR InterPro: IPR002335; Myoglobin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PRINTS: PR00613; MYOGLOBIN.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 FT NON_TER 142 142
 SQ SEQUENCE 142 AA: 15481 MW: 64D14BC6C16AB2 CRC64;

Query Match 100.0%; Score 10; DB 6; Length 142;
 Best Local Similarity 100.0%; Pred. No. 6.7e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10
 DB 33 LVVYPTQRF 42

RESULT 21
 ID 013071 PRELIMINARY; PRT; 142 AA.
 AC 013071;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE EPSILON-GLOBIN (FRAGMENT).
 OS Callithrix geoffroyi (Geoffroy's marmoset).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
 OX NCBI_TaxID=52231;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98121278; PubMed=9461380;
 RA Porter C.A., Czelusniak J., Schneider H., Schneider M.P., Sampalo I.,
 RA Goodman M.;
 RT "Sequences of the primate epsilon-globin gene: implications for
 systematics of the marmosets and other New World primates."
 RL Gene 205:59-71(1997).
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: U97029; AAC39572.1; -.
 DR HSSP: P02100; 1A9W.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR InterPro: IPR002335; Myoglobin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PRINTS: PR00613; MYOGLOBIN.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 FT NON_TER 142 142
 SQ SEQUENCE 142 AA: 15522 MW: 8A5480BC2F5BCC4 CRC64;

Query Match 100.0%; Score 10; DB 6; Length 142;
 Best Local Similarity 100.0%; Pred. No. 6.7e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10
 DB 33 LVVYPTQRF 42

RESULT 22

O9GJY8
 ID 09GJY8 PRELIMINARY; PRT; 145 AA.
 AC 09GJY8;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE GAMMA2-GLOBIN.
 GN GAMMA2-GLOBIN.
 OS Callipebus molloch (Dusky titl).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Callicebinae;
 OC Callipebus.
 OX NCBI_TaxID=9523;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98121277; PubMed=9461379;
 RA Chiu C.H., Schneider H., Slightom J.L., Gumucio D.L., Goodman M.;
 RT "Dynamics of regulatory evolution in primate beta-globin gene
 clusters: cis-mediated acquisition of simian gamma fetal expression
 patterns."
 RT patterns."
 RL Gene 205:47-57(1997).
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: AF321379; AAG35072.1; -.
 DR HSSP: P02096; 1FDH.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 SQ SEQUENCE 145 AA: 15757 MW: FA329002D22C37C8 CRC64;

Query Match 100.0%; Score 10; DB 6; Length 145;
 Best Local Similarity 100.0%; Pred. No. 6.8e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10
 DB 33 LVVYPTQRF 42

RESULT 23
 ID 028460 PRELIMINARY; PRT; 146 AA.
 AC 028460;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE UNKNOWN PROTEIN (FRAGMENT).
 OS Microtus angustirostris (Northern elephant seal).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Plimipedia; Phocidae; Microtus.
 OX NCBI_TaxID=9716;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Larick J.W., Espinoza D.O., Coloma M.J., Le Boeuf B.J.;
 RT "Alpha and beta-globin sequences of the northern elephant seal
 (Mirounga angustirostris)."
 RT Submitted (FEB-1992) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: M73997; AAA30963.1; -.
 DR HSSP: P02023; 1BAH.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR InterPro: IPR002335; Myoglobin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PRINTS: PR00613; MYOGLOBIN.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 FT NON_TER 1 1
 SQ SEQUENCE 146 AA: 16044 MW: 2543427BF15A711A CRC64;

Query Match 100.0%; Score 10; DB 6; Length 146;
 Best Local Similarity 100.0%; Pred. No. 6.9e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
 |||||
 DB 32 LVVYPWTQRF 41

RESULT 24

O9BX96

ID O9BX96 PRELIMINARY; PRT; 147 AA.

AC O9BX96; 01-JUN-2001 (TREMblrel. 17, Created)

DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)

DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)

DE BETA GLOBIN CHAIN VARIANT.

GN HBB.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Blood;

RA Kutlar F., Holley L., Leithner C., Kutlar A.;

RT "A rare beta chain variant 'Hemoglobin Ty Gard:Pro 124 Gln' found in a

RT Caucasian female with erythrocytosis."

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

DR EMBL: AF349114; AKK29639.1; -.

DR HSSP: P02023; IDXT.

DR InterPro: IPR002337; Beta_haem.

DR InterPro: IPR000971; Globin.

DR InterPro: IPR002335; Myoglobin.

DR Pfam: PF00042; globin; 1.

DR PRINTS: PR00814; BETAHAEM.

DR PRINTS: PR00613; MYOGLOBIN.

DR PROSITE: PS01033; GLOBIN; 1.

KM Erythrocyte; Heme; Oxygen transport; Respiratory protein.

FT VARIANT 125 125 0 -> P.

SQ SEQUENCE 147 AA; 16013 MW; F35A79221C65577A CRC64;

Query Match 100.0%; Score 10; DB 4; Length 147;
 Best Local Similarity 100.0%; Pred. No. 6.9e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
 |||||
 DB 33 LVVYPWTQRF 42

RESULT 25

O96FH7

ID O96FH7 PRELIMINARY; PRT; 147 AA.

AC O96FH7; 01-DEC-2001 (TREMblrel. 19, Created)

DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)

DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)

DE SIMILAR TO HEMOGLOBIN, GAMMA A.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=BONE MARROW, AND CHRONIC MYELOGENOUS LEUKEMIA;

RA Strausberg R.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC010913; AAH10913.1; -.

SQ SEQUENCE 147 AA; 16128 MW; 0CEAD9E932416DCF CRC64;

Query Match 100.0%; Score 10; DB 4; Length 147;
 Best Local Similarity 100.0%; Pred. No. 6.9e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
 |||||
 DB 33 LVVYPWTQRF 42

RESULT 26

O96FH6

ID O96FH6 PRELIMINARY; PRT; 147 AA.

AC O96FH6; 01-DEC-2001 (TREMblrel. 19, Created)

DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)

DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)

DE SIMILAR TO HEMOGLOBIN, GAMMA G.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=BONE MARROW, AND CHRONIC MYELOGENOUS LEUKEMIA;

RA Strausberg R.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC010914; AAH10914.1; -.

SQ SEQUENCE 147 AA; 16126 MW; 8FCDC4441BA16DDE CRC64;

Query Match 100.0%; Score 10; DB 4; Length 147;
 Best Local Similarity 100.0%; Pred. No. 6.9e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
 |||||
 DB 33 LVVYPWTQRF 42

RESULT 27

O29415

ID O29415 PRELIMINARY; PRT; 147 AA.

AC O29415; 01-NOV-1996 (TREMblrel. 01, Created)

DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)

DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)

DE Epsilon-GLOBIN SUBUNIT.

OS Cebus olivaceus (Weeper capuchin), and

OS Cebus kaapori.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Cebus.

OX NCBI_TaxID=37295, 37294;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=LYMPHOCYTES;

RX MEDLINE=96111507; Pubmed=8845968;

RA Harada M.L., Schneider H., Schneider M.P., Sampaio I., Czelusniak J.,

RA Goodman M.; "DNA evidence on the phylogenetic systematics of New World monkeys:

RT support for the sister-grouping of Cebus and Saimiri from two unlinked

RT nuclear genes."

RL MOL. Phylogenet. Evol. 4:331-349(1995).

CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

DR EMBL: U18610; AAB40982.1; -.

DR EMBL: U18608; AAB40981.1; -.

DR HSSP: P02100; 1A9W.

DR InterPro: IPR002337; Beta_haem.

DR InterPro: IPR000971; Globin.

DR Pfam: PF00042; globin; 1.

DR PRINTS: PR00814; BETAHAEM.

DR PROSITE: PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
SQ SEQUENCE 147 AA; 16320 MW; 5EF74B18BD314E22 CRC64;

Query Match 100.0%; Score 10; DB 6; Length 147;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10
| | | | | | | | | |
DB 33 LVVYPTQRF 42

RESULT 28
OQ3901 PRELIMINARY; PRT; 147 AA.
AC Q03901;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BETA GLOBIN.
OS Galago crassicaudatus (Thick-tailed galago) (Otolemur crassicaudatus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirrhini; Galagonidae; Otolemur.
OX NCBI_TaxID=9463;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91210254; PubMed=2019578;
RA Tagle D.A., Slightom J.L., Jones R.T., Goodman M.;
RT "Concerted evolution led to high expression of a prosimian primate
delta globin gene locus."
RL J. Biol. Chem. 266:7469-7480(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=LIVER;
RC MEDLINE=92347874; PubMed=1639402;
RA Tagle D.A., Stanhope M.J., Stemieniak D.R., Benson P., Goodman M.,
RA Slightom J.L.;
RT "The beta globin gene cluster of the prosimian primate Galago
crassicaudatus: nucleotide sequence determination of the 41-kb cluster
and comparative sequence analyses."
RL Genomics 13:741-760(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Slightom J.L.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL; M61740; AAA35445.1; -;
DR EMBL; U60902; AAC50963.1; -;
DR HSSP; P02023; IDXT.
DR InterPro; IPR002337; Beta_haem.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin.1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
SQ SEQUENCE 147 AA; 16085 MW; 2AC69646BD001B5 CRC64;

Query Match 100.0%; Score 10; DB 6; Length 147;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10
| | | | | | | | | |
DB 33 LVVYPTQRF 42

RESULT 29
OQ3903 PRELIMINARY; PRT; 147 AA.
ID OQ3903

AC Q03903;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HEMOGLOBIN GAMMA-2(A).
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnivora; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91334472; PubMed=1908094;
RA Fitch D.H., Bailey W.J., Tagle D.A., Goodman M., Sten L.,
RA Slightom J.L.;
RT "Duplication of the gamma-globin gene mediated by L1 long interspersed
repetitive elements in an early ancestor of simian primates."
RL Proc. Natl. Acad. Sci. U.S.A. 88:7396-7400(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88315036; PubMed=3410846;
RA Slightom J.L., Koop B.F., Xu P., Goodman M.;
RT "Rhesus fetal globin genes. Concerted gene evolution in the descent of
higher primates."
RL J. Biol. Chem. 263:12427-12438(1988).
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL; X53419; CAA37498.1; -;
DR EMBL; M19433; AAA36845.1; -;
DR HSSP; P02096; IEDH.
DR InterPro; IPR002337; Beta_haem.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin.1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
SQ SEQUENCE 147 AA; 16127 MW; 8854449B26B9D97F CRC64;

Query Match 100.0%; Score 10; DB 6; Length 147;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10
| | | | | | | | | |
DB 33 LVVYPTQRF 42

RESULT 30
OQ6J57 PRELIMINARY; PRT; 147 AA.
AC OQ6J57;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GAMMA1-GLOBIN (GAMMA2-GLOBIN).
GN GAMMA1-GLOBIN.
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callitrix.
OX NCBI_TaxID=9483;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98121277; PubMed=9461379;
RA Chiu C.H., Schneider H., Slightom J.L., Gunnucio D.L., Goodman M.;
RT "Dynamics of regulatory evolution in primate beta-globin gene
clusters: cis-mediated acquisition of simian gamma fetal expression
patterns."
RL Gene 205:47-57(1997).
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL; AF016991; AAC33930.1; -;
DR EMBL; AF016991; AAC33930.1; -;
DR HSSP; P02096; IEDH.
DR InterPro; IPR002337; Beta_haem.

DR InterPro: IPR000971; Globin.
 DR InterPro: IPR002335; Myoglobin.
 DR Pfam: PF00042; globin. 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PRINTS: PR00613; MYOGLOBIN.
 DR PROSITE: PS01033; GLOBIN. 1.
 DR Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 SQ SEQUENCE 147 AA; 15980 MW; 8A6417F8C5F2FB17 CRC64;

Query Match 100.0%; Score 10; DB 6; Length 147;
 Best Local Similarity 100.0%; Pred. No. 6.9e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
 DB 33 LVVYPWTORE 42

RESULT 31
 O9GLX7 PRELIMINARY; PRT; 147 AA.

AC O9GLX7; 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HYBRID GAMMA1/GAMMA2-GLOBIN.
 OS Salimiri sciureus (Common squirrel monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Salimiri.
 OX NCBI_TaxID=9521;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98121277; PubMed=9461379;
 RA Chiu C.H., Schneider H., Slightom J.L., Guncuio D.L., Goodman M.;
 RT "Dynamics of regulatory evolution in primate beta-globin gene
 RT clusters: cis-mediated acquisition of simian gamma fetal expression
 RT patterns.";
 RL Gene 205:47-57(1997).
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL; AF016983; AAG33925.1; -.
 DR HSSP; P02096; 1PDH.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR InterPro: IPR002335; Myoglobin.
 DR Pfam; PF00042; globin. 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PRINTS: PR00613; MYOGLOBIN.
 DR PROSITE: PS01033; GLOBIN. 1.
 DR Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 SQ SEQUENCE 147 AA; 15925 MW; 01F417F8D0593E26 CRC64;

Query Match 100.0%; Score 10; DB 6; Length 147;
 Best Local Similarity 100.0%; Pred. No. 6.9e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
 DB 33 LVVYPWTORE 42

RESULT 32
 O9GLX6 PRELIMINARY; PRT; 147 AA.

AC O9GLX6; 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HYBRID GAMMA1/GAMMA2-GLOBIN.
 OS Salimiri ustus (Squirrel monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Salimiri.

OX NCBI_TaxID=66265;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98121277; PubMed=9461379;
 RA Chiu C.H., Schneider H., Slightom J.L., Guncuio D.L., Goodman M.;
 RT "Dynamics of regulatory evolution in primate beta-globin gene
 RT clusters: cis-mediated acquisition of simian gamma fetal expression
 RT patterns.";
 RL Gene 205:47-57(1997).
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL; AF016984; AAG33926.1; -.
 DR HSSP; P02096; 1PDH.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR InterPro: IPR002335; Myoglobin.
 DR Pfam; PF00042; globin. 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PRINTS: PR00613; MYOGLOBIN.
 DR PROSITE: PS01033; GLOBIN. 1.
 DR Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 SQ SEQUENCE 147 AA; 15957 MW; 01F417F8C1582E26 CRC64;

Query Match 100.0%; Score 10; DB 6; Length 147;
 Best Local Similarity 100.0%; Pred. No. 6.9e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
 DB 33 LVVYPWTORE 42

RESULT 33
 O9GLX5 PRELIMINARY; PRT; 147 AA.

AC O9GLX5; 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HYBRID GAMMA1/GAMMA2-GLOBIN.
 OS Aotus nancymae (Owl monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
 OX NCBI_TaxID=37293;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98121277; PubMed=9461379;
 RA Chiu C.H., Schneider H., Slightom J.L., Guncuio D.L., Goodman M.;
 RT "Dynamics of regulatory evolution in primate beta-globin gene
 RT clusters: cis-mediated acquisition of simian gamma fetal expression
 RT patterns.";
 RL Gene 205:47-57(1997).
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL; AF016985; AAG33927.1; -.
 DR HSSP; P02096; 1PDH.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR InterPro: IPR002335; Myoglobin.
 DR Pfam; PF00042; globin. 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PRINTS: PR00613; MYOGLOBIN.
 DR PROSITE: PS01033; GLOBIN. 1.
 DR Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 SQ SEQUENCE 147 AA; 15896 MW; B5F417E9944F60FB CRC64;

Query Match 100.0%; Score 10; DB 6; Length 147;
 Best Local Similarity 100.0%; Pred. No. 6.9e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
 DB 33 LVVYPWTORE 42

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RESULT 34
ID 028779 PRELIMINARY: PRT: 147 AA.
AC 028779;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE DNA.
OS Pan paniscus (Pygmy chimpanzee) (Bonobo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxID=9597;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94115696; PubMed=1342932;
RA Bailey W.J., Hayasaka K., Skinner C.G., Kehoe S., Siew L.C.,
RA Silghom J.L., Goodman M.;
RT "Reexamination of the African hominoid trichotomy with additional
RT sequences from the primate beta-globin gene cluster.";
RL Mol. Phylogenet. Evol. 1:97-135(1992).
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL; M93716; AAA72113.1; -.
DR HSSP; P02096; 1PDH.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin.1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
SQ SEQUENCE 147 AA; 16168 MW; 8FCD1527AC6DDE CRC64;

Query Match 100.0%; Score 10; DB 6; Length 147;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
Db 33 LVVYPWTORE 42

RESULT 35
ID 088752 PRELIMINARY: PRT: 147 AA.
AC 088752;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE EPSILON 1 GLOBIN.
CN EPSILON 1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=41STAR;
RA Hirotsuki S.;
RL Submitted (AUG-1990) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=41STAR;
RA MEDLINE=99214072; PubMed=10196478;
RA Sato H., Inokuchi N., Nagae Y., Okazaki T.;
RT "Molecular cloning and characterization of two sets of alpha-theta
RT genes in the rat alpha-like globin gene cluster.";
RL Gene 230:91-99(1999).
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL; X56326; CA39765.1; -.
DR HSSP; P02100; 1A9W.
DR InterPro: IPR002337; Beta_haem.

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DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin.1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
SQ SEQUENCE 147 AA; 16104 MW; 1C264EC1AF5C58E CRC64;

Query Match 100.0%; Score 10; DB 11; Length 147;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
Db 33 LVVYPWTORE 42

RESULT 36
ID 014491 PRELIMINARY: PRT: 152 AA.
AC 014491;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HEMOGLOBIN GAMMA-G (FRAGMENT).
CN HBG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8123783; PubMed=7250702;
RA Cavalliesco C., Forget B.G., derfel J.K., Wilson L.B., Wilson J.T.,
RA Weissman S.M.;
RT "Nucleotide sequence of human G gamma globin messenger RNA.";
RL Gene 12:215-221(1980).
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL; M15386; AAB50159.1; -.
DR HSSP; P02096; 1PDH.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR InterPro: IPR002335; Myoglobin.
DR Pfam: PF00042; globin.1.
DR PRINTS: PR00814; BETAHAEM.
DR PRINTS: PR00613; MYOGLOBIN.
DR PROSITE: PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
FT NON_TER 1
SQ SEQUENCE 152 AA; 16594 MW; F13FF666EECE879 CRC64;

Query Match 100.0%; Score 10; DB 4; Length 152;
Best Local Similarity 100.0%; Pred. No. 7.1e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
Db 38 LVVYPWTORE 47

RESULT 37
ID 014403 PRELIMINARY: PRT: 155 AA.
AC 014403;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GAMMA-G GLOBIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;

```

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LIVER:
 RA Vladimir V., Kavan V.M.;
 RL Submitted (SEP-1990) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LIVER:
 RA Dmitrenko V.V., Kavan V.M.;
 RT "Nucleotide sequence of mitochondrial cytochrome c oxidase II from
 human fetal liver."
 RL Submitted (MAY-1992) to the EMBL/Genbank/DBJ databases.
 CC -I- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: X55656; CA39189.1; -.
 DR HSSP: P02096; IFDH.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR InterPro: IPR002335; Myoglobin.
 DR Pfam: PF00042; globin.1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PRINTS: PR00613; MYOGLOBIN.
 DR PROSITE: PS01033; GLOBIN.1.
 DR Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 FT NON_TER 1
 SQ SEQUENCE 155 AA; 16969 MW; FEB0151ABAA4B6EF CRC64;

Query Match 100.0%; Score 10; DB 4; Length 155;
 Best Local Similarity 100.0%; Pred. No. 7.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
 Db 26 LVVYPWTQRF 35

RESULT 38
 ID 014473 PRELIMINARY; PRT; 175 AA.
 AC 014473;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE BETA-GLOBIN GENE FROM A THALASSEMIA PATIENT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=9025169; PubMed=1971109;
 RA Thein S.L., Hesketh C., Taylor P., Temperley I.J., Hutchinson R.M.,
 RA Old J.N., Wood W.G., Clegg J.B., Weatherall D.J.;
 RT "Molecular basis for dominantly inherited inclusion body beta-
 thalassemia."
 RL Proc. Natl. Acad. Sci. U.S.A. 87:3924-3928(1990).
 CC -I- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: M34059; AAA35952.1; -.
 DR EMBL: M34058; AAA35952.1; JOINED.
 DR HSSP: P02023; IDXT.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin.1.
 DR PROSITE: PS01033; GLOBIN.1.
 DR Heme; Oxygen transport; Respiratory protein.
 SQ SEQUENCE 175 AA; 18931 MW; E87DDB659A3E950 CRC64;

Query Match 100.0%; Score 10; DB 4; Length 175;
 Best Local Similarity 100.0%; Pred. No. 7.9e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
 Db 26 LVVYPWTQRF 35

Db 33 LVVYPWTQRF 42
 RESULT 39
 ID 09BEH6 PRELIMINARY; PRT; 52 AA.
 AC 09BEH6;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE OMEGA GLOBIN (FRAGMENT).
 OS Trichosurus vulpecula (Brush-tailed possum).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprodontia; Phalangeridae; Trichosurus.
 OX NCBI_TaxID=9337;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21107677; PubMed=1158601;
 RA Wheeler D., Hope R., Cooper S.J., Dolman G., Webb G.C., Bottema C.D.,
 RA Cooley A.A., Goodman M., Holland R.A.;
 RT "An orphaned mammalian beta-globin gene of ancient evolutionary
 origin."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:1101-1106(2001).
 CC -I- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: AY014775; AAK11490.1; -.
 DR HSSP: P02118; 1A4F.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin.1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN.1.
 DR Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 52 AA; 5736 MW; CD90D13786E59037 CRC64;

Query Match 90.0%; Score 9; DB 6; Length 52;
 Best Local Similarity 100.0%; Pred. No. 0.00047;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 9
 Db 13 LVVYPWTQRF 21

RESULT 40
 ID 061650 PRELIMINARY; PRT; 52 AA.
 AC 061650;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE BETA-GLOBIN (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=80132479; PubMed=7357610;
 RA Pavlakis G.N., Lockard R.E., Vamvakopoulos N., Rieser L.,
 RA Rajbhandary U.L., Vournakis J.N.;
 RT "Secondary structure of mouse and rabbit alpha- and beta-globin mRNAs:
 RT differential accessibility of alpha and beta initiator AUG codons
 towards nucleases."
 RL Cell 19:91-102(1980).
 CC -I- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: M10524; AAA37785.1; -.
 DR HSSP: P02023; IDXT.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin.1.
 DR PROSITE: PS01033; GLOBIN.1.

KW Heme; Oxygen transport; Respiratory protein.
RT NON_TER 52
SQ SEQUENCE 52 AA; 5690 MW; 99899C3C3D71EA34 CRC64;

Query Match 90.0%; Score 9; DB 11; Length 52;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQR 9
| | | | | | | | | |
DB 33 LVVYPWTQR 41

RESULT 41
Q9BEH8 PRELIMINARY; PRT; 54 AA.
AC Q9BEH8;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE OMEGA GLOBIN (FRAGMENT).
OS Dasyurus viverrinus (Southeastern quoll).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Dasyuromorpha; Dasyuridae; Dasyurus.
OC NCBI_TaxID=9279;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21107677; PubMed=11158601;
RA Wheeler D., Hope R., Cooper S.J., Dolman G., Webb G.C., Bottema C.D.,
RA Gooley A.A., Goodman M., Holland R.A.;
RT "An orphaned mammalian beta-globin gene of ancient evolutionary
origin."
RL Proc. Natl. Acad. Sci. U.S.A. 98:1101-1106(2001).
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL: AY014773; AAK11488.1; -.
DR HSSP: P02118; 1A4F.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
FT NON_TER 1
SQ SEQUENCE 54 AA; 6059 MW; 9D370673E475C499 CRC64;

Query Match 90.0%; Score 9; DB 6; Length 54;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQR 9
| | | | | | | | | |
DB 21 LVVYPWTQR 29

RESULT 42
Q9BEH9 PRELIMINARY; PRT; 58 AA.
AC Q9BEH9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE OMEGA GLOBIN (FRAGMENT).
OS Macropus giganteus (Eastern gray kangaroo).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OC NCBI_TaxID=9317;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21107677; PubMed=11158601;
RA Wheeler D., Hope R., Cooper S.J., Dolman G., Webb G.C., Bottema C.D.,

RA Gooley A.A., Goodman M., Holland R.A.;
RT "An orphaned mammalian beta-globin gene of ancient evolutionary
origin."
RL Proc. Natl. Acad. Sci. U.S.A. 98:1101-1106(2001).
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL: AY014772; AAK11487.1; -.
DR HSSP: P02118; 1A4F.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
FT NON_TER 1
SQ SEQUENCE 58 AA; 6390 MW; 3B4A24F723D2BC2A CRC64;

Query Match 90.0%; Score 9; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00052;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQR 9
| | | | | | | | | |
DB 19 LVVYPWTQR 27

RESULT 43
Q9BXM3 PRELIMINARY; PRT; 59 AA.
AC Q9BXM3;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE TRUNCATED BETA-GLOBIN.
GN HBB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang Z., Chu J., Ban G., Lin K., Shi L., Tao Y., Sun H.;
RT "Molecular characterization of beta thalassaemia in Yunnan, China."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL: AF319479; AAK28066.1; -.
DR HSSP: P02023; IDXT.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PROSITE: PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Respiratory protein.
SQ SEQUENCE 59 AA; 6542 MW; 84936430BD1E09F1 CRC64;

Query Match 90.0%; Score 9; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.00052;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQR 9
| | | | | | | | | |
DB 33 LVVYPWTQR 41

RESULT 44
Q9BEH7 PRELIMINARY; PRT; 60 AA.
AC Q9BEH7;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE OMEGA GLOBIN (FRAGMENT).
OS Peromyscus gunnisoni (Eastern barred bandicoot).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Peramelemorphia; Peramelidae; Perameles.
OX NCBI_TaxID=37737;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=21107677; PubMed=11158601;
RA Wheeler D., Hope R., Cooper S.J., Dolman G., Webb G.C., Bottema C.D.,
RA Cooley A.A., Goodman M., Holland R.A.;
RT "An orphaned mammalian beta-globin gene of ancient evolutionary
origin."
RL Proc. Natl. Acad. Sci. U.S.A. 98:1101-1106(2001).
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL: AY014774; AAK11469.1; -
DR HSSP: P02118; 14AF.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
KM Erythrocyte; Heme; Oxygen transport; Respiratory protein.
FT NON_TER 1 1
SQ SEQUENCE 60 AA; 6585 MW; 6FA8AF6123F2CE7 CRC64;

Query Match 90.0%; Score 9; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTWQR 9
DB 21 LVVYPTWQR 29

RESULT 45
O9CR22 PRELIMINARY; PRT; 134 AA.
AC O9CR22;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 13 DAYS EMBRYO LIVER CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE CLONE:251004007, FULL INSERT SEQUENCE (FRAGMENT).
GN HBB-B1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=EMBRYONIC LIVER;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiba H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

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DR EMBL: AK011075; BAB27380.1; -
DR HSSP: P02023; 1BAB.
DR MGD: MGI:96021; Hbb-b1.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR InterPro: IPR002335; Myoglobin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00814; BETAHAEM.
DR PRINTS: PR00613; MYOGLOBIN.
DR PROSITE: PS01033; GLOBIN; 1.
KM Erythrocyte; Heme; Oxygen transport; Respiratory protein.
FT NON_TER 1 1
SQ SEQUENCE 134 AA; 14394 MW; A92A8CBBE8231F29 CRC64;

Query Match 90.0%; Score 9; DB 11; Length 134;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTWQR 9
DB 20 LVVYPTWQR 28

RESULT 46
O9QW91 PRELIMINARY; PRT; 146 AA.
AC O9QW91;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BETA 2 GLOBIN.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN (1)
RP SEQUENCE.
RX MEDLINE=94185903; PubMed=8138033;
RX Ferranti P., Carbone V., Sannolo N., Flume I., Malorni A.;
RT "Mass spectrometric analysis of rat hemoglobin by FAB-overlapping.
RT Primary structure of the alpha-major and of four beta constitutive
RT chains."
RL Int. J. Biochem. 25:1943-1950(1993).
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR HSSP: P02023; 1BAB.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR InterPro: IPR002335; Myoglobin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00814; BETAHAEM.
DR PRINTS: PR00613; MYOGLOBIN.
DR PROSITE: PS01033; GLOBIN; 1.
KM Erythrocyte; Heme; Oxygen transport; Respiratory protein.
SQ SEQUENCE 146 AA; 15847 MW; 3E071113CC957725 CRC64;

Query Match 90.0%; Score 9; DB 11; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTWQR 9
DB 32 LVVYPTWQR 40

RESULT 47
O9QUT6 PRELIMINARY; PRT; 146 AA.
AC O9QUT6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

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DE BETA 1 GLOBIN.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94185903; PubMed=8138033;
RA Ferranti P., Carbone V., Sannolo N., Piume I., Malorni A.;
RT "Mass spectrometric analysis of rat hemoglobin by FAB-overlapping,
RT primary structure of the alpha-major and of four beta constitutive
RT chains";
RL Int. J. Biochem. 25:1943-1950(1993).
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR HSSP; P02023; 1BAB.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR InterPro: IPR002335; Myoglobin.
DR Pfam: PF00042; globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PRINTS; PR00613; MYOGLOBIN.
DR PROSITE; PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
SQ SEQUENCE 146 AA; 15834 MW; 3E04BF5C8757D23 CRC64;

Query Match 90.0%; Score 9; DB 11; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVYPTWTOR 9
Db 32 LVYPTWTOR 40
IIIIIIII

RESULT 48
O9QUN8 PRELIMINARY; PRT; 146 AA.
ID O9QUN8;
AC O9QUN8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BETA-2-GLOBIN (FRAGMENT).
GN HBB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9373250; PubMed=10441738;
RA Ueda Y., Miyashita N., Imai K., Yamaguchi Y., Takamura K.,
RA Notohara M., Shirolshi T., Kawashima T., Ning L., Wang C., Wu X.,
RA Moriwaki K.;
RT "Nucleotide sequences of the mouse globin beta gene cDNAs in a wild
RT derived new haplotype Hbwl";
RL Mamm. Genome 10:879-882(1999).
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL; AB020016; BAA77356.1; -;
DR EMBL; AB020014; BAA77354.1; -;
DR HSSP; P02023; 1BAB.
DR MGD; MGI:96020; Hbb.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR InterPro: IPR002335; Myoglobin.
DR Pfam: PF00042; globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PRINTS; PR00613; MYOGLOBIN.
DR PROSITE; PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
FT NON_TER 1
SQ SEQUENCE 146 AA; 15703 MW; 566D816A91C5F0FD CRC64;

Query Match 90.0%; Score 9; DB 11; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVYPTWTOR 9
Db 32 LVYPTWTOR 40
IIIIIIII

RESULT 49
O9ROS6 PRELIMINARY; PRT; 146 AA.
ID O9ROS6;
AC O9ROS6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BETA-1-GLOBIN (FRAGMENT).
GN HBB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9373250; PubMed=10441738;
RA Ueda Y., Miyashita N., Imai K., Yamaguchi Y., Takamura K.,
RA Notohara M., Shirolshi T., Kawashima T., Ning L., Wang C., Wu X.,
RA Moriwaki K.;
RT "Nucleotide sequences of the mouse globin beta gene cDNAs in a wild
RT derived new haplotype Hbwl";
RL Mamm. Genome 10:879-882(1999).
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL; AB020013; BAA77353.1; -;
DR HSSP; P02023; 1BAB.
DR MGD; MGI:96020; Hbb.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR InterPro: IPR002335; Myoglobin.
DR Pfam: PF00042; globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PRINTS; PR00613; MYOGLOBIN.
DR PROSITE; PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
FT NON_TER 1
SQ SEQUENCE 146 AA; 15709 MW; 7C4504C326D197A5 CRC64;

Query Match 90.0%; Score 9; DB 11; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVYPTWTOR 9
Db 32 LVYPTWTOR 40
IIIIIIII

RESULT 50
O9BEI2 PRELIMINARY; PRT; 147 AA.
ID O9BEI2;
AC O9BEI2;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE OMEGA GLOBIN.
OS Macropus eugenii (Tamar wallaby).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21107677; PubMed=11158601;
RA Wheeler D., Hope R., Cooper S.J., Dolman G., Webb G.C., Boltema C.D.,

RA Gooley A.A., Goodman M., Holland R.A.;
 RT "An orphaned mammalian beta-globin gene of ancient evolutionary
 origin";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:1101-1106(2001).
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: AY014769; AAK11484.1; -.
 DR HSSP: P02112; 1HBR.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR InterPro: IPR002335; Myoglobin.
 DR Pfam: PF00042; globin.1.
 DR PRINTS: PR00814; MYOGLOBIN.
 DR PRINTS: PR00613; MYOGLOBIN.
 DR PROSITE: PS01033; GLOBIN.1.
 KM Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 SQ SEQUENCE 147 AA; 16108 MW; 54AD783F0B5BF488 CRC64;

Query Match 90.0%; Score 9; DB 6; Length 147;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTOR 9
 |||||
 Db 33 LVVYPWTOR 41

RESULT 51
 Q9BE11 PRELIMINARY; PRT; 147 AA.
 AC Q9BE11;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE OMEGA GLOBIN.
 OS Smittinopsis crassicaudata (Fat-tailed dunnart).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Smittinopsis.
 OX NCBI_TaxID=9301;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21107677; PubMed=1158601;
 RA Wheeler D., Hope R., Cooper S.J., Dolman G., Webb G.C., Bottema C.D.,
 RA Gooley A.A., Goodman M., Holland R.A.;
 RT "An orphaned mammalian beta-globin gene of ancient evolutionary
 origin";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:1101-1106(2001).
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: AY014770; AAK11485.1; -.
 DR HSSP: P02112; 1HBR.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR InterPro: IPR002335; Myoglobin.
 DR Pfam: PF00042; globin.1.
 DR PRINTS: PR00814; MYOGLOBIN.
 DR PRINTS: PR00613; MYOGLOBIN.
 DR PROSITE: PS01033; GLOBIN.1.
 KM Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 SQ SEQUENCE 147 AA; 16350 MW; 47510F7C2D569B74 CRC64;

Query Match 90.0%; Score 9; DB 6; Length 147;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTOR 9
 |||||
 Db 33 LVVYPWTOR 41

RESULT 52
 Q9CY54 PRELIMINARY; PRT; 147 AA.
 ID Q9CY54

AC Q9CY54;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE HEMOGLOBIN, BETA ADULT MAJOR CHAIN.
 GN HBB-B1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC LIVER;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai T., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirral L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Blake J., Boffelli D., Botjunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilming L.,
 RA Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: AK010873; BAB27237.1; -.
 DR HSSP: P02023; 1DXT.
 DR MGD; MGI:96021; Hbb-b1.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR InterPro: IPR002335; Myoglobin.
 DR Pfam: PF00042; globin.1.
 DR PRINTS: PR00814; MYOGLOBIN.
 DR PRINTS: PR00613; MYOGLOBIN.
 DR PROSITE: PS01033; GLOBIN.1.
 KM Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 SQ SEQUENCE 147 AA; 15778 MW; 79E4AFBEAE95972 CRC64;

Query Match 90.0%; Score 9; DB 11; Length 147;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTOR 9
 |||||
 Db 33 LVVYPWTOR 41

RESULT 53
 Q9CY12 PRELIMINARY; PRT; 147 AA.
 ID Q9CY12;
 AC Q9CY12;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE 13 DAYS EMBRYO LIVER CDNA, RIKEN FULL-LENGTH ENRICHD LIBRARY,
 DE CLONE:2510039D09, FULL INSERT SEQUENCE.
 GN HBB-B1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6J: TISSUE-EMBRYONIC LIVER;
 RX MEDLINE-21085660; PubMed-11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Atzawa K., Izawa M., Nishi K., Kiyosawa H., Konno S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Glisli C., King B., Kochia H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsch G.,
 RA Blake J., Boileau D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinac S., Hill D., Hofmann M., Hume D.A., Kamaya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Saeki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyoko-Oka K., Wang K.H., Wetz C., Whitaker C., Wilmink L.,
 RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC EMBL: AK011053; BAB27362.1; -
 DR HSP: P02023; IDXT.
 DR MGD: MGI:96021; Hbb-b1.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR InterPro: IPR002335; Myoglobin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; MYOGLOBIN.
 DR PROSITE: PS01033; GLOBIN.1.
 RX Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 SO SEQUENCE 147 AA; 15763 MW; 6CF0FC2FA2A929 CRC64;

Query Match 90.0%; Score 9; DB 11; Length 147;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVYPTPTOR 9
 DB 33 LVYPTPTOR 41

Q91V86 PRELIMINARY: PRT: 147 AA.
 Q91V86;

DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE 11 DAYS EMBRYO CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
 DE CLONE:2700082N11, FULL INSERT SEQUENCE (ADULT MALE KIDNEY CDNA, RIKEN
 DE FULL-LENGTH ENRICHED LIBRARY, CLONE:0610006005, FULL INSERT SEQUENCE)
 DE (ADULT MALE KIDNEY CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
 DE CLONE:0610009619, FULL INSERT SEQUENCE) (ADULT MALE SPLEEN CDNA, RIKEN
 DE FULL-LENGTH ENRICHED LIBRARY, CLONE:0910001914, FULL INSERT SEQUENCE)
 DE (18 DAYS EMBRYO CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
 DE CLONE:1110005K11, FULL INSERT SEQUENCE) (ADULT FEMALE PLACENTA CDNA,
 DE RIKEN FULL-LENGTH ENRICHED LIBRARY, CLONE:1600013K09, FULL INSERT
 DE SEQUENCE) (ADULT FEMALE PLACENTA CDNA, RIKEN FULL-LENGTH ENRICHED
 DE LIBRARY, CLONE:1600019A13, FULL INSERT SEQUENCE) (ADULT FEMALE
 DE PLACENTA CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY, CLONE:1600019I13,
 DE FULL INSERT SEQUENCE) (13 DAYS EMBRYO LIVER CDNA, RIKEN FULL-LENGTH
 DE ENRICHED LIBRARY, CLONE:2510004F04, FULL INSERT SEQUENCE) (13 DAYS
 DE EMBRYO LIVER CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
 DE CLONE:2510019E11, FULL INSERT SEQUENCE) (13 DAYS EMBRYO LIVER CDNA,
 DE RIKEN FULL-LENGTH ENRICHED LIBRARY, CLONE:2510019H05, FULL INSERT
 DE SEQUENCE) (13 DAYS EMBRYO LIVER CDNA, RIKEN FULL-LENGTH ENRICHED
 DE LIBRARY, CLONE:2510022J06, FULL INSERT SEQUENCE) (13 DAYS EMBRYO LIVER

DE CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY, CLONE:2510023M22, FULL
 DE INSERT SEQUENCE) (13 DAYS EMBRYO LIVER CDNA, RIKEN FULL-LENGTH
 DE ENRICHED LIBRARY, CLONE:2510027H07, FULL INSERT SEQUENCE) (13 DAYS
 DE EMBRYO LIVER CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
 DE CLONE:2510028E09, FULL INSERT SEQUENCE) (13 DAYS EMBRYO LIVER CDNA,
 DE RIKEN FULL-LENGTH ENRICHED LIBRARY, CLONE:2510028J08, FULL INSERT
 DE SEQUENCE) (13 DAYS EMBRYO LIVER CDNA, RIKEN FULL-LENGTH ENRICHED
 DE LIBRARY, CLONE:2510029L07, FULL INSERT SEQUENCE) (13 DAYS EMBRYO LIVER
 DE CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY, CLONE:2510031C09, FULL
 DE INSERT SEQUENCE) (13 DAYS EMBRYO LIVER CDNA, RIKEN FULL-LENGTH
 DE ENRICHED LIBRARY, CLONE:2510039C10, FULL INSERT SEQUENCE) (13 DAYS
 DE EMBRYO LIVER CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
 DE CLONE:2510039D08, FULL INSERT SEQUENCE) (13 DAYS EMBRYO LIVER CDNA,
 DE RIKEN FULL-LENGTH ENRICHED LIBRARY, CLONE:2510039M06, FULL INSERT
 DE SEQUENCE) (13 DAYS EMBRYO LIVER CDNA, RIKEN FULL-LENGTH ENRICHED
 DE LIBRARY, CLONE:2510040I07, FULL INSERT SEQUENCE) (13 DAYS EMBRYO LIVER
 DE CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY, CLONE:2510040K10, FULL
 DE INSERT SEQUENCE) (13 DAYS EMBRYO LIVER CDNA, RIKEN FULL-LENGTH
 DE ENRICHED LIBRARY, CLONE:2510040P08, FULL INSERT SEQUENCE) (13 DAYS
 DE EMBRYO LIVER CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
 DE CLONE:2510041H16, FULL INSERT SEQUENCE) (13 DAYS EMBRYO LIVER CDNA,
 DE RIKEN FULL-LENGTH ENRICHED LIBRARY, CLONE:2510044F14, FULL INSERT
 DE SEQUENCE).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6J: TISSUE-KIDNEY, SPLEEN, PLACENTA, AND LIVER;
 RA Adachi J., Atzawa K., Akahira S., Akimura T., Aono H., Arai A.,
 RA Arakawa T., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
 RA Imocani K., Ishii Y., Itoh M., Izawa M., Kato H., Kawai J., Kojima Y.,
 RA Komono H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T.,
 RA Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D.,
 RA Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y.,
 RA Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y.,
 RA Toyu T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (Jul-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6J: TISSUE-KIDNEY, SPLEEN, PLACENTA, AND LIVER;
 RX MEDLINE-21085660; PubMed-11217851;
 RA RIKEN PANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6J: TISSUE-KIDNEY, SPLEEN, PLACENTA, AND LIVER;
 RX MEDLINE-99279253; PubMed-10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6J: TISSUE-KIDNEY, SPLEEN, PLACENTA, AND LIVER;
 RX MEDLINE-20499374; PubMed-11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6J: TISSUE-KIDNEY, SPLEEN, PLACENTA, AND LIVER;
 RX MEDLINE-20530913; PubMed-11076661;
 RA Shibata K., Itoh M., Atzawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Shihata K., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama N., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Matakiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN Integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.",
 RL Genome Res. 10:1757-1771(2000).
 DR EMBL: AK012551; BAB28311.1; -
 DR EMBL: AK002258; BAB21971.1; -
 DR EMBL: AK003394; BAB22067.1; -
 DR EMBL: AK003096; BAB22562.1; -
 DR EMBL: AK003472; BAB22806.1; -
 DR EMBL: AK005442; BAB24036.1; -
 DR EMBL: AK005490; BAB24075.1; -
 DR EMBL: AK005496; BAB24080.1; -
 DR EMBL: AK010902; BAB27255.1; -
 DR EMBL: AK010980; BAB27302.1; -
 DR EMBL: AK010981; BAB27303.1; -
 DR EMBL: AK010991; BAB27310.1; -
 DR EMBL: AK010993; BAB27312.1; -
 DR EMBL: AK011006; BAB27325.1; -
 DR EMBL: AK011013; BAB27331.1; -
 DR EMBL: AK011016; BAB27334.1; -
 DR EMBL: AK011027; BAB27343.1; -
 DR EMBL: AK011033; BAB27347.1; -
 DR EMBL: AK011050; BAB27360.1; -
 DR EMBL: AK011052; BAB27361.1; -
 DR EMBL: AK011057; BAB27365.1; -
 DR EMBL: AK011067; BAB27374.1; -
 DR EMBL: AK011069; BAB27376.1; -
 DR EMBL: AK011077; BAB27382.1; -
 DR EMBL: AK011083; BAB27387.1; -
 DR EMBL: AK011102; BAB27399.1; -
 SQ SEQUENCE 147 AA; 15748 MW; 6CFOEABEFLF3EB9D CRC64;

Query Match 90.0%; Score 9; DB 11; Length 147;
 Best Local Similarity 100.0%; Pred. No. 0.0011;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTOR 9
 |||||
 Db 33 LVVYPWTOR 41

RESULT 55
 O9YGF5 PRELIMINARY; PRT; 147 AA.
 AC O9YGF5;
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE EMBRYONIC BETA-TYPE GLOBIN.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maruyama K.;
 RT "Rainbow Trout Embryonic beta-Type Globin";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: AB015450; BAA34950.1; -
 DR HSSP: P80044; 1PBX.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR InterPro: IPR002335; Myoglobin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PRINTS: PR00613; MYOGLOBIN.
 DR PROSITE: PS01033; GLOBIN; 1.
 KM Erythrocyte; Heme; Oxygen transport; Respiratory protein.

SQ SEQUENCE 147 AA; 16396 MW; 79EB74B4EFAA13EA CRC64;

Query Match 90.0%; Score 9; DB 13; Length 147;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTOR 9
 |||||
 Db 33 LVVYPWTOR 41

RESULT 56
 O98UB9 PRELIMINARY; PRT; 147 AA.
 AC O98UB9;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE BETANCP1.
 GN BETANCP1.
 OS Notothenia coriiceps (black rockcod).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
 OC Notothenioidae; Nototheniidae; Notothenia.
 OX NCBI_TaxID=8208;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cocca E., Detrich H.W. III, Parker S.K., di Prisco G.;
 RT "A cluster of four globin genes from the Antarctic fish Notothenia
 RT coriiceps";
 RL J. Fish Biol. 57:33-50(2000).
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: AF230741; AAK12632.1; -
 DR HSSP: P80044; 1PBX.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR InterPro: IPR002335; Myoglobin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PRINTS: PR00613; MYOGLOBIN.
 DR PROSITE: PS01033; GLOBIN; 1.
 KM Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 SQ SEQUENCE 147 AA; 16556 MW; 6CEC71C7B8A8C094 CRC64;

Query Match 90.0%; Score 9; DB 13; Length 147;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTOR 9
 |||||
 Db 33 LVVYPWTOR 41

RESULT 57
 O98UB8 PRELIMINARY; PRT; 147 AA.
 AC O98UB8;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE BETANCP2.
 GN BETANCP2.
 OS Notothenia coriiceps (black rockcod).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
 OC Notothenioidae; Nototheniidae; Notothenia.
 OX NCBI_TaxID=8208;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Cocco E., Detrich H.W. III, Parker S.K., di Prisco G.,
 RT "A cluster of four globin genes from the Antarctic fish Notothenia
 coriiceps".
 RL J. Fish Biol. 57:33-50(2000).
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: AF230741; AK12630.1; -.
 DR HSSP: P80044; 1PBX.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 SQ SEQUENCE 147 AA; 16481 MW; 4AA39E1EC1BC89DE CRC64;

Query Match 90.0%; Score 9; DB 13; Length 147;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTWTOR 9
 |||||
 DB 33 LVVYPTWTOR 41

RESULT 58
 OQCXZ2 PRELIMINARY: PRT: 163 AA.
 AC OQCXZ2:
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE 13 DAYS EMBRYO LIVER CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
 DE CLONE:2510049H02, FULL INSERT SEQUENCE.
 GN HBB-B1
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC LIVER;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi S., Yamakata I.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka T.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
 RA Kuehl P., Lewis S., Matsuo Y., Mikalido I., Pesole G., Quackenbush J.,
 RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai J., Boffelli D., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofman M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Norioka P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyokawa K., Wang K.H., Weltz C., Wittaker C., Wilming L.,
 RA Wyszynski A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: AK011119; BAB27413.1; -.
 DR HSSP: P02023; 1DXT.
 DR MGD: MGI:96021; Hbb-b1.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.

SQ SEQUENCE 163 AA; 17403 MW; D024994DF19CD71E CRC64;

Query Match 90.0%; Score 9; DB 11; Length 163;
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTWTOR 9
 |||||
 DB 33 LVVYPTWTOR 41

RESULT 59
 O90594 PRELIMINARY: PRT: 15 AA.
 ID O90594:
 AC O90594:
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-JAN-1999 (TREMBLrel. 09, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE GLOBIN (FRAGMENT).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81261952; PubMed=6266925;
 RA Padayatty J., Cummings I., Manske C.L., Higuchi R., Woe S., Salser W.;
 RT "Cloning of chicken globin cDNA in bacterial plasmids";
 RL Gene 13:417-422(1981).
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: M10380; AAA48803.1; -.
 DR InterPro: IPR000971; Globin.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Respiratory protein.
 FT NON_TER 1 1
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1881 MW; 23E61DA734FA7962 CRC64;

Query Match 80.0%; Score 8; DB 13; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.0027;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 VYPTWDRF 10
 |||||
 DB 6 VYPTWDRF 13

RESULT 60
 O9BE10 PRELIMINARY: PRT: 31 AA.
 ID O9BE10:
 AC O9BE10:
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE OMEGA GLOBIN (FRAGMENT).
 OS Monodelphis domestica (short-tailed grey opossum).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
 OX NCBI_TaxID=13616;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21107677; PubMed=11158601;
 RA Wheeler D., Hope R., Cooper S.J., Dolman G., Webb G.C., Bottema C.D.,
 RA Gooley A.A., Goodman M., Holland R.A.;
 RT "An orphaned mammalian beta-globin gene of ancient evolutionary
 origin";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:1101-1106(2001).
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: AY014771; AK11486.1; -.
 DR HSSP: P02096; 1FDH.

DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin. 1.
 DR PROSITE: PS01033; GLOBIN. 1.
 KW Heme; Oxygen transport; Respiratory protein.
 FT NON_TER 1 31
 FT NON_TER 1 31
 SQ SEQUENCE 31 AA; 3547 MW; 0353D72F3681617D CRC64;

Query Match 80.0%; Score 8; DB 6; Length 31;
 Best Local Similarity 100.0%; Pred. No. 0.005;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVPTQ 8
 DB 24 LVVPTQ 31

RESULT 61
 ID 099M06 PRELIMINARY; PRT; 61 AA.
 AC 099M06;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
 DE ADULT BETA MAJOR GLOBIN (FRAGMENT).
 OS Crictulus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Crictulus.
 OX NCBI_TaxID=10029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2136356; PubMed=11470818;
 RA Li F., Chen J., Izumi M., Butler M.C., Keizer S.M., Gilbert D.M.;
 RT "The replication timing program of the Chinese hamster beta-globin
 RT locus is established coincident with its repositioning near peripheral
 RT heterochromatin in early G1 phase.";
 RL J. Cell Biol. 154:283-292(2001).
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL; AF314661; AAK19259.1; -.
 DR HSSP; P02023; 1ABW.
 DR InterPro: IPR002337; Beta.haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam; PF00042; globin. 1.
 DR PRINTS; PR00814; BETAHAEM.
 DR PROSITE; PS01033; GLOBIN. 1.
 KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 FT NON_TER 1 61
 FT NON_TER 1 61
 SQ SEQUENCE 61 AA; 6801 MW; 7B6DC974B31348FC CRC64;

Query Match 80.0%; Score 8; DB 11; Length 61;
 Best Local Similarity 100.0%; Pred. No. 0.0087;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 VYPWTOF 10
 DB 4 VYPWTOF 11

RESULT 62
 ID 064372 PRELIMINARY; PRT; 73 AA.
 AC 064372;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
 DE (DEER MOUSE) BETA-2-GLOBIN (HBB-B2) DNA, SECOND CODING-BLOCK REGION,
 DE PARTIAL CDS (FRAGMENT).
 OS Peromyscus maniculatus (Deer mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
 OC Peromyscus.
 OX NCBI_TaxID=10042;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88188975; PubMed=3447002;
 RA Padgett R.W., Loeb D.D., Snyder L.R.G., Edgell M.H.,
 RA Hutchison C.A. III;
 RT "The molecular organization of the beta-globin complex of the deer
 RT mouse, Peromyscus maniculatus.";
 RL Mol. Biol. Evol. 4:30-45(1987).
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL; M15295; AAA40594.1; -.
 DR EMBL; M15294; AAA40593.1; -.
 DR HSSP; P02070; 1HDA.
 DR InterPro: IPR002337; Beta.haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam; PF00042; globin. 1.
 DR PRINTS; PR00814; BETAHAEM.
 DR PROSITE; PS01033; GLOBIN. 1.
 KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 FT NON_TER 1 73
 FT NON_TER 1 73
 SQ SEQUENCE 73 AA; 8095 MW; C7E033D2FE913292 CRC64;

Query Match 80.0%; Score 8; DB 11; Length 73;
 Best Local Similarity 100.0%; Pred. No. 0.01;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 VYPWTOF 10
 DB 4 VYPWTOF 11

RESULT 63
 ID 062586 PRELIMINARY; PRT; 73 AA.
 AC 062586;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
 DE (DEER MOUSE) BETA-3-GLOBIN (HBB-B3) DNA, SECOND CODING-BLOCK REGION
 DE (FRAGMENT).
 OS Peromyscus maniculatus (Deer mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
 OC Peromyscus.
 OX NCBI_TaxID=10042;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88188975; PubMed=3447002;
 RA Padgett R.W., Loeb D.D., Snyder L.R.G., Edgell M.H.,
 RA Hutchison C.A. III;
 RT "The molecular organization of the beta-globin complex of the deer
 RT mouse, Peromyscus maniculatus.";
 RL Mol. Biol. Evol. 4:30-45(1987).
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL; M15296; AAA40595.1; -.
 DR HSSP; P02070; 1HDA.
 DR InterPro: IPR002337; Beta.haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam; PF00042; globin. 1.
 DR PRINTS; PR00814; BETAHAEM.
 DR PROSITE; PS01033; GLOBIN. 1.
 KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 FT NON_TER 1 73
 FT NON_TER 1 73
 SQ SEQUENCE 73 AA; 8081 MW; 04E04BC921413F1A CRC64;

Query Match 80.0%; Score 8; DB 11; Length 73;
 Best Local Similarity 100.0%; Pred. No. 0.01;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VYPWTORF 10
|||||

Db 4 VYPWTORF 11

RESULT 64
ID 099M07 PRELIMINARY; PRT; 75 AA.

AC 099M07;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE B-LIKE Y-GLOBIN (FRAGMENT).
GN B-LIKE Y-GLOBIN.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=2136356; Pubmed=11470818;
RA Li F., Chen J., Izumi M., Butler M.C., Keezer S.M., Gilbert D.M.;
RT "The replication timing program of the Chinese hamster beta-globin
locus is established coincident with its repositioning near peripheral
heterochromatin in early G1 phase."
RL J. Cell Biol. 154:283-292(2001).
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL: AF314659; AAK20665.1; -
DR EMBL: AF314658; AAK20665.1; JOINED.
DR HSSP: P02096; 1FDH.
DR InterPro: IPR002337; Beta.haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin.1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN.1.
KM Erythrocyte; Heme; Oxygen transport; Respiratory protein.
FT NON_TER 1 1
FT NON_TER 75 75
SQ SEQUENCE 75 AA; 828 MW; BA5D98B8AE52E0 CRC64;

Query Match 80.0%; Score 8; DB 11; Length 75;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VYPWTORF 10
|||||

Db 33 VYPWTORF 40

RESULT 65

ID 09XT23 PRELIMINARY; PRT; 106 AA.

AC 09XT23;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE EPSILON GLOBIN (FRAGMENT).
OS Cercariae; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium.
OX NCBI_TaxID=9807;
RN [1]

RP SEQUENCE FROM N.A.
RA Kim G., Kim S.J., Ryder O.A., Oh M.Y.;
RT "Phylogenetic relationship of the Perissodactyla group using epsilon
globin gene and their gene highly conserved."
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DE EMBL: AF139502; AAD39938.1; -

DR HSSP: P02100; 1A9W.
DR InterPro: IPR002337; Beta.haem.
DR InterPro: IPR000971; Globin.
DR InterPro: IPR002335; Myoglobin.
DR Pfam: PF00042; globin.1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; MYOGLOBIN.
DR PROSITE: PS01033; GLOBIN.1.
KM Erythrocyte; Heme; Oxygen transport; Respiratory protein.
FT NON_TER 106 106
SQ SEQUENCE 106 AA; 11652 MW; B7EB74AA13012B1F CRC64;

Query Match 80.0%; Score 8; DB 6; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQ 8
|||||

Db 33 LVVYPWTQ 40

RESULT 65
ID 09XT22 PRELIMINARY; PRT; 106 AA.

AC 09XT22;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE EPSILON GLOBIN (FRAGMENT).
OS Taptirus terrestris (Lowland tapir) (Brazilian tapir).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Tapiridae; Taptirus.
OX NCBI_TaxID=9801;
RN [1]

RP SEQUENCE FROM N.A.
RA Kim G., Kim S.J., Ryder O.A., Oh M.Y.;
RT "Phylogenetic relationship of the Perissodactyla group using epsilon
globin gene and their gene highly conserved."
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL: AF139503; AAD39939.1; -
DR HSSP: P02100; 1A9W.
DR InterPro: IPR002337; Beta.haem.
DR InterPro: IPR000971; Globin.
DR InterPro: IPR002335; Myoglobin.
DR Pfam: PF00042; globin.1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; MYOGLOBIN.
DR PROSITE: PS01033; GLOBIN.1.
KM Erythrocyte; Heme; Oxygen transport; Respiratory protein.
FT NON_TER 106 106
SQ SEQUENCE 106 AA; 11652 MW; B7EB74AA13012B1F CRC64;

Query Match 80.0%; Score 8; DB 6; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQ 8
|||||

Db 33 LVVYPWTQ 40

RESULT 67

ID 095183 PRELIMINARY; PRT; 106 AA.

AC 095183;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE EPSILON-1 GLOBIN (FRAGMENT).
GN EPSILON-1.

OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CHEJU NATIVE HORSE;
 RA Kim G.O., Kim S.J., Kim K.I., Oh M.Y.;
 RT "Isolation and characterization of epsilon-1 gene in Cheju native horse."
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: U70986; AAB16849.1; -
 DR HSSP: P02100; 1A9W.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR InterPro: IPR002335; Myoglobin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PRINTS: PR00613; MYOGLOBIN.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 FT NON_TER 106 106
 SQ SEQUENCE 106 AA; 11663 MW; B7EED10B53A48B1F CRC64;
 OY 1 LVYVPMTO 8
 Db 33 LVYVPMTO 40
 RESULT 68
 OQCZG2 PRELIMINARY; PRT; 125 AA.
 AC OQCZG2;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE 10, 11 DAYS EMBRYO CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
 DE CLONE:2810003C03, FULL INSERT SEQUENCE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
 RX MEDLINE=21085660; Pubmed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Konde S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasuawa T., Saito R.,
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carinci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Segs T., Shibata Y., Storch K.-F.,
 RA Suzuki K., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

DR EMBL: AK012654; BAB28385.1; -
 DR HSSP: P02100; 1A9W.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 SQ SEQUENCE 125 AA; 14198 MW; 8CAED0F8CBA64C235 CRC64;
 OY 3 VYPWTORE 10
 Db 35 VYPWTORE 42
 RESULT 69
 OQCZG2 PRELIMINARY; PRT; 135 AA.
 AC OQCZG2;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE BETA-GLOBIN CHAIN (FRAGMENT).
 GN BETA-HL-R.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WISTAR;
 RA Stevanovic M.J., Crkvenjakov R.;
 RL Submitted (JUN-1991) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: X60730; CAA43138.1; -
 DR HSSP: P02100; 1A9W.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR InterPro: IPR002335; Myoglobin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PRINTS: PR00613; MYOGLOBIN.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 FT NON_TER 135 135
 SQ SEQUENCE 135 AA; 15257 MW; 2C776CF27A9FDE27 CRC64;
 OY 3 VYPWTORE 10
 Db 35 VYPWTORE 42
 RESULT 70
 OQCZG2 PRELIMINARY; PRT; 140 AA.
 AC OQCZG2;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE BETA-H1-GLOBIN (FRAGMENT).
 GN HBB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

ID 088753 PRELIMINARY; PRT; 147 AA.
AC 088753;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
GN EPSILON 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR;
RA Hirayuki S.;
RL Submitted (Aug-1990) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR;
RX MEDLINE=99214072; PubMed=10196478;
RT Sato H., Inokuchi N., Nagae Y., Okazaki T.;
RT "Molecular cloning and characterization of two sets of alpha-theta
RT genes in the rat alpha-like globin gene cluster.";
RL Gene 230:91-99(1999).
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL: X56327; CAA39766.1; -.
DR HSSP: P02100; 1A9W.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
SQ SEQUENCE 147 AA; 16388 MW; 8F83E066420FA56 CRC64;

Query Match 80.0%; Score 8; DB 11; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VYPMWTORF 10
Db 35 VYPMWTORF 42
RESULT 74
ID 088754 PRELIMINARY; PRT; 147 AA.
AC 088754;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
GN EPSILON 3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR;
RA Hirayuki S.;
RL Submitted (Aug-1990) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR;
RX MEDLINE=99214072; PubMed=10196478;
RT Sato H., Inokuchi N., Nagae Y., Okazaki T.;
RT "Molecular cloning and characterization of two sets of alpha-theta
RT genes in the rat alpha-like globin gene cluster.";
RL Gene 230:91-99(1999).
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL: X56328; CAA39767.1; -.

DR HSSP: P02100; 1A9W.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
SQ SEQUENCE 147 AA; 16540 MW; 39BF594C21B3DC1E CRC64;

Query Match 80.0%; Score 8; DB 11; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VYPMWTORF 10
Db 35 VYPMWTORF 42

RESULT 75
ID 063067 PRELIMINARY; PRT; 147 AA.
AC 063067;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
GN BETA-GLOBIN CHAIN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR;
RA Stevanovic M.J., Crkvenjakov R.;
RL Submitted (JUN-1991) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL: X60729; CAA43137.1; -.
DR HSSP: P02096; 1FDH.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
SQ SEQUENCE 147 AA; 16452 MW; EE75C2674642446B CRC64;

Query Match 80.0%; Score 8; DB 11; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VYPMWTORF 10
Db 35 VYPMWTORF 42

RESULT 76
ID 090864 PRELIMINARY; PRT; 147 AA.
AC 090864;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
GN BETA-H GLOBIN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE-94140361; PubMed-8307571;
 RA Reisman M., Grasso J.A., Blumenthal R., Levitt P.;
 RT "Primary sequence, evolution, and repetitive elements of the Gallus
 gallus (chicken) beta-globin cluster.";
 CC Genomics 18:616-626(1993).
 RL -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: L17432; AAD03346.1; -;
 DR HSSP: P02112; 1HBR.
 DR InterPro: IPR002337; Beta_haem.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 SO SEQUENCE 147 AA; 16365 MW; C933A2810304AD9C CRC64;

Query Match 80.0%; Score 8; DB 13; Length 147;
 Best Local Similarity 100.0%; Pred. No. 0.018;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 VYPWTORE 10
 |||||
 DB 35 VYPWTORE 42

RESULT 77

ID Q90938 PRELIMINARY; PRT; 147 AA.

AC Q90938; 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE MRNA, COMPLETE ORF.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RA Larrick J.W., Espinoza D.O.;

RT "Mutant hemoglobin (Beta chain thr 69->ser) with high oxygen affinity

RL Submitted (JAN-1992) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

DR EMBL: M73995; AAA48996.1; -;

DR HSSP: P02112; 1HBR.

DR InterPro: IPR002337; Beta_haem.

DR Pfam: PF00042; globin; 1.

DR PRINTS: PR00814; BETAHAEM.

DR PROSITE: PS01033; GLOBIN; 1.

KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.

SO SEQUENCE 147 AA; 16452 MW; F0E3972C6DE73428 CRC64;

Query Match 80.0%; Score 8; DB 13; Length 147;
 Best Local Similarity 100.0%; Pred. No. 0.018;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 VYPWTORE 10
 |||||
 DB 35 VYPWTORE 42

RESULT 78

ID Q95408 PRELIMINARY; PRT; 57 AA.

AC Q95408; 01-MAY-1999 (TREMBlrel. 10, Created)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE BETA GLOBIN (FRAGMENT).
 GN HBB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BLOOD;
 RA Kuttar F., Wilson J., Wenk R.E., Luddy R., Holley L., Markowitz R.,
 RT "Hemoglobin Sinai-Greenspring, a new silent GTC 34 ATC mutation of
 human beta globin gene.";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: AF104901; AAC9372.1; -;
 DR HSSP: P02023; 1DXT.
 DR InterPro: IPR002337; Beta_haem.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 FT VARIANT 35 57
 FT NON_TER 57 57
 SO SEQUENCE 57 AA; 6266 MW; FDC12A13AD35934 CRC64;

Query Match 70.0%; Score 7; DB 4; Length 57;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 VYPWTORE 10
 |||||
 DB 36 VYPWTORE 42

RESULT 79

ID Q9PWH7 PRELIMINARY; PRT; 69 AA.

AC Q9PWH7; 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE SB-H2. GLOBIN (FRAGMENT).

OS Morone saxatilis (Striped bass).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidae;

OC Moronidae; Morone.

OX NCBI_TaxID=34816;

RN [1]

RP SEQUENCE FROM N.A.

RA Hirono I., Aoki T., Powers D.A.;

RT "Characterization of the alpha and beta globin genes of striped bass,

RT Morone saxatilis.";

RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

DR EMBL: AB023443; BAA82806.1; -;

DR HSSP: P80044; 1HBR.

DR InterPro: IPR002337; Beta_haem.

DR Pfam: PF00042; globin; 1.

DR PRINTS: PR00814; BETAHAEM.

DR PROSITE: PS01033; GLOBIN; 1.

KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.

FT NON_TER 1 69

SO SEQUENCE 69 AA; 7715 MW; AA489EABEAB55E0E CRC64;

Query Match 70.0%; Score 7; DB 13; Length 69;

Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VYPMTOR 9
Db 2 VYPMTOR 8

RESULT 80

09PMH5 ID 09PMH5 PRELIMINARY; PRT; 69 AA.
AC 09PMH5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE BETA GLOBIN (FRAGMENT).
GN SB-B4.
OS Morone saxatilis (Striped bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciforma; Perciformes; Percoidae;
OC Moronidae; Morone.
OX NCBI_TaxID=34816;
RN [1]
RA Hirono I., Aoki T., Powers D.A.;
RT "Characterization of the alpha and beta globin genes of striped bass,
Morone saxatilis."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL: AB023445; BAA82808.1; -
DR HSSP: P80044; 1HBB.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
FT NON_TER 1 1
FT NON_TER 69 69
SQ SEQUENCE 69 AA; 7767 MW; 0B6B5B632991C1CA CRC64;

Query Match 70.0%; Score 7; DB 13; Length 69;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VYPMTOR 9
Db 2 VYPMTOR 8

RESULT 81

090488 ID 090488 PRELIMINARY; PRT; 105 AA.
AC 090488;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE BETA GLOBIN (FRAGMENT).
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RA SEQUENCE FROM N.A.
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL: U50382; AAB05405.1; -
DR HSSP: P56251; 1SPG.
DR InterPro: IPR002337; Beta_haem.

DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
FT NON_TER 105 105
SQ SEQUENCE 105 AA; 11689 MW; 8CBB8D5377D99D9C CRC64;

Query Match 70.0%; Score 7; DB 13; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VYPMTOR 9
Db 35 VYPMTOR 41

RESULT 82

063011 ID 063011 PRELIMINARY; PRT; 146 AA.
AC 063011;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE ZERO BETA-GLOBIN (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RA SEQUENCE FROM N.A.
RX MEDLINE=95130713; PubMed=7829656;
RA Inokuchi N.;
RT "Isolation and characterization of three rat adult type beta-globin
genes."
RL Nippon Ika Daigaku Zasshi 61:620-632(1994).
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL: S74802; AAC60699.1; -
DR HSSP: P02023; 1BAB.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
FT NON_TER 1 1
SQ SEQUENCE 146 AA; 15906 MW; 06FA5FE1C78AFF6 CRC64;

Query Match 70.0%; Score 7; DB 11; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VYPMTOR 9
Db 34 VYPMTOR 40

RESULT 83

09D0B2 ID 09D0B2 PRELIMINARY; PRT; 147 AA.
AC 09D0B2;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE HEMOGLOBIN Y, BETA-LIKE EMBRYONIC CHAIN.
GN HBB-Y.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6J; TISSUE-EMBRYO;
 RX MEDLINE-21085660; PubMed-11217851;
 RA Kawai J., Shlnagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Alizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fletschmann W., Gaasterland T., Gissi C., King B., Koehli H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikiado I., Pesole G., Quackenbush J.,
 RA Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein S., Hill D., Hofmann M., Hume D.A., Kamya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,
 RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyoko-Oka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
 RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsuki S.,
 RA Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: AK011619; BAB27738.1; -;
 DR HSSP: P02100; 1A9W.
 DR MGD: MGI:96027; Hbb-Y.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR InterPro: IPR002335; Myoglobin.
 DR Pfam: PF00042; globin.1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS00613; MYOGLOBIN.
 DR PROSITE: PS01033; GLOBIN.1.
 DR Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 SQ SEQUENCE 147 AA; 16073 MW; 21D5C09E559709B4 CRC64;

Query Match 70.0%; Score 7; DB 11; Length 147;
 Best Local Similarity 100.0%; Pred. No. 0.29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVYPT 7
 |||||||
 Db 33 LVVYPT 39

RESULT 84
 O9CR49 PRELIMINARY; PRT; 147 AA.
 AC O9CR49;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE HEMOGLOBIN Y, BETA-LIKE EMBRYONIC CHAIN.
 GN HBB-Y.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6J; TISSUE-EMBRYO;
 RX MEDLINE-21085660; PubMed-11217851;
 RA Kawai J., Shlnagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Alizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fletschmann W., Gaasterland T., Gissi C., King B., Koehli H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikiado I., Pesole G., Quackenbush J.,
 RA Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein S., Hill D., Hofmann M., Hume D.A., Kamya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,
 RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyoko-Oka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
 RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsuki S.,
 RA Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: AK012897; BAB28541.1; -;
 DR EMBL: AK012501; BAB28284.1; -;
 DR HSSP: P02100; 1A9W.
 DR MGD: MGI:96027; Hbb-Y.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR InterPro: IPR002335; Myoglobin.
 DR InterPro: IPR001032; Plant_globin.
 DR Pfam: PF00042; globin.1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PRINTS: PR00613; MYOGLOBIN.
 DR PROSITE: PS00188; PLANTGLOBIN.
 DR PROSITE: PS01033; GLOBIN.1.
 DR Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 SQ SEQUENCE 147 AA; 16146 MW; 21D6767F697583B4 CRC64;

Query Match 70.0%; Score 7; DB 11; Length 147;
 Best Local Similarity 100.0%; Pred. No. 0.29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVYPT 7
 |||||||
 Db 33 LVVYPT 39

RESULT 85
 O62669 PRELIMINARY; PRT; 147 AA.
 AC O62669;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE ZERO BETA-1 GLOBIN.
 GN 0 BETA-1 GLOBIN.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-WISTAR; TISSUE-LIVER;
 RA Inokuchi N., Iwahara S.I., Satoh H., Nagoe Y., Okazaki T.;
 RA "Organization structure and expression of rat beta-globin genes.";
 RL Submitted (JUL-1992) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: X67611; CAA47872.1; -;
 DR EMBL: X67612; CAA47872.1; JOINED.
 DR HSSP: P02023; 1DXT.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin.1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN.1.
 KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 SQ SEQUENCE 147 AA; 16022 MW; 4A11053B63C53F50 CRC64;

Query Match 70.0%; Score 7; DB 11; Length 147;
 Best Local Similarity 100.0%; Pred. No. 0.29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 VYPMTOR 9
 DB 35 VYPMTOR 41

RESULT 86

062670 PRELIMINARY: PRT: 147 AA.
 AC 062670;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE 0 BETA-2 GLOBIN.
 GN 0 BETA-2 GLOBIN.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=MTSTAR; TISSUE=LIVER;
 RA Inouchi N., Iwahara S.I., Satoh H., Nagoe Y., Okazaki T.;
 RT "Organization structure and expression of rat beta-globin genes";
 RL Submitted (JUL-1992) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: X67617; CAA47877.1; -.
 DR HSSP: P02023; IDXT.
 DR InterPro: IPR002337; Beta.haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin.1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN.1.
 DR Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 KW SEQUENCE 147 AA; 15979 MW; 93BB045CC26D57BA CRC64;
 SQ

Query Match 70.0%; Score 7; DB 11; Length 147;
 Best Local Similarity 100.0%; Pred. No. 0.29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 VYPMTOR 9
 DB 35 VYPMTOR 41

RESULT 87

091470 PRELIMINARY: PRT: 147 AA.
 AC 091470; O13233; O13185;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
 DE BETA-GLOBIN.
 OS Salmo salar (Atlantic salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
 OX NCBI_TaxID=8030;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96211166; PubMed-8924215;
 RA McMorow T., Wagner A., Deryckere F., Gannon F.;
 RT "Structural organization and sequence analysis of the globin locus in Atlantic salmon."
 RL DNA Cell Biol. 15:407-414(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-97311408; PubMed-9168125;
 RA McMorow T., Wagner A., Harle T., Gannon F.;
 RT "Sequence analysis and tissue expression of a non-bohr beta-globin cDNA from Atlantic salmon."
 RL Gene 189:183-188(1997).

CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

DR EMBL: X97289; CAA65953.1; -.
 DR EMBL: Y08923; CAA70128.1; -.
 DR HSSP: P02142; 100T.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin.1.
 DR PROSITE: PS01033; GLOBIN.1.
 KW Heme; Oxygen transport; Respiratory protein.
 SQ SEQUENCE 147 AA; 15985 MW; 20469DCE4E575F44 CRC64;

Query Match 70.0%; Score 7; DB 13; Length 147;
 Best Local Similarity 100.0%; Pred. No. 0.29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 VYPMTOR 9
 DB 35 VYPMTOR 41

RESULT 88

09YGF4 PRELIMINARY: PRT: 147 AA.
 AC 09YGF4;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAY-2001 (TREMBLrel. 19, Last annotation update)
 DE EMBRYONIC BETA-TYPE GLOBIN2.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maruyama K.;
 RT "Rainbow Trout Embryonic beta-Type Globin2";
 RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: AB015451; BAA34951.1; -.
 DR HSSP: P80044; 1PBX.
 DR InterPro: IPR002337; Beta.haem.
 DR InterPro: IPR000971; Globin.
 DR InterPro: IPR002335; Myoglobin.
 DR Pfam: PF00042; globin.1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PRINTS: PR00613; MYOGLOBIN.
 DR PROSITE: PS01033; GLOBIN.1.
 DR Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 KW SEQUENCE 147 AA; 16655 MW; D7CBCC5F971762E8 CRC64;
 SQ

Query Match 70.0%; Score 7; DB 13; Length 147;
 Best Local Similarity 100.0%; Pred. No. 0.29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 VYPMTOR 9
 DB 35 VYPMTOR 41

RESULT 89

09PVL8 PRELIMINARY: PRT: 147 AA.
 AC 09PVL8;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE LARVAL BETA-GLOBIN.
 OS Hynobius retardatus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Cryptobranchioidea; Hynobidae; Hynobius.
 OX NCBI_TaxID=36312;

[1]
RN SEQUENCE FROM N.A.
RA Yamaguchi M., Takahashi H., Makahara M.;
RT "Erythropoiesis and unexpected expression pattern of globin genes in
the salamander *Hynobius retardatus*.";
RL Dev. Genes Evol. 0:0-0(1999).
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL: AB034757; BAA86390.1; -.
DR HSSP: P02118; 1A4F.
DR InterPro: IPR002337; Beta.haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
SQ SEQUENCE 147 AA; 16006 MW; A96F1D05A4AD4727 CRC64;

Query Match 70.0%; Score 7; DB 13; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 VYPWTOR 9
DB 35 VYPWTOR 41

RESULT 90
O93548 PRELIMINARY; PRT; 147 AA.
AC O93548;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE EMBRYONIC 1 BETA-GLOBIN.
GN BEL.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99147139; PubMed=10022956;
RA Quinkert A., Campos-Ortega J.A.;
RT "A new beta-globin gene from the zebrafish, *beta1*, and its pattern of
transcription during embryogenesis.";
RL Dev. Genes Evol. 209:126-131(1999).
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL: AF082662; AAC62069.1; -.
DR HSSP: P80044; 1PBX.
DR InterPro: IPR002337; Beta.haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
SQ SEQUENCE 147 AA; 16162 MW; D972A74BD71F717 CRC64;

Query Match 70.0%; Score 7; DB 13; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 VYPWTOR 9
DB 35 VYPWTOR 41

RESULT 91
O91A59 PRELIMINARY; PRT; 147 AA.
ID O91A59;
AC O91A59;

DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BETA GLOBIN.
OS *Notothernia angustata* (Rockcod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Nototheniidae; Notothenidae; Notothenia.
OX NCBI_TaxID=8210;
RN [1]
RP SEQUENCE FROM N.A.
RA Lau D.T., Saeed A., Parker S.K., Detrich H.W. III.;
RT "Divergent Transcription of the 5'-to-5' Linked Adult alpha- and
beta-globin Genes of the Antarctic Teleost *Notothernia coriiceps* Is
Controlled by Dual Promoters and Intergenic Enhancers.";
RL Submitted (Sep-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL: AF187046; AAF36818.1; -.
DR HSSP: P80044; 1PBX.
DR InterPro: IPR002337; Beta.haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
SQ SEQUENCE 147 AA; 16200 MW; 615CB02EB04009F4 CRC64;

Query Match 70.0%; Score 7; DB 13; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 VYPWTOR 9
DB 35 VYPWTOR 41

RESULT 92
O91471 PRELIMINARY; PRT; 147 AA.
ID O91471;
AC O91471;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BETA-GLOBIN.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Proteanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96211166; PubMed=8924215;
RA McMorrow T., Wagner A., Deryckere F., Gannon F.;
RT "Structural organisation and sequence analysis of the globin locus
from Atlantic salmon.";
RL DNA Cell Biol. 15:407-414(1996).
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL: X97287; CAA65950.1; -.
DR HSSP: P02142; 1OUT.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PROSITE: PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Respiratory protein.
SQ SEQUENCE 147 AA; 15971 MW; CD5F5BE1F9060E19 CRC64;

Query Match 70.0%; Score 7; DB 13; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 VYPWTOR 9

Db 35 VYPWTOR 41

RESULT 93

ID 091129 PRELIMINARY; PRT; 147 AA.

AC 091129;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE BETA-GLOBIN.
OS Notothenia coriiceps (black rockcod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Nototheniidae; Notothenidae; Notothenia.
OX NCBI_TaxID=8208;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95199244; PubMed=7892183;
RA Cocco E., Ratnayake-Iecamasam M., Parker S.K., Camardella L.,
RA Claramella M., di Prisco G., Detrich H.W. III;
RT "Genomic remnants of alpha-globin genes in the hemoglobinless
RT antarctic icefishes."
RL Proc. Natl. Acad. Sci. U.S.A. 97:1817-1821(1995).
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL; 009187; AAC60372.1; -;
DR HSSP; P80044; IPBX.
DR InterPro; IPR002337; Beta.haem.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PRINTS; PRO0814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
SQ SEQUENCE 147 AA; 16316 MW; 966A33B9878D5D22 CRC64;

Query Match 70.0%; Score 7; DB 13; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 VYPWTOR 9
Db 35 VYPWTOR 41

RESULT 94

ID 0902M4 PRELIMINARY; PRT; 147 AA.

AC 0902M4;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HEMOGLOBIN BETA CHAIN.
OS Epinephelus coioides (orange-spotted grouper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Seranidae; Epinephelus.
OX NCBI_TaxID=94232;
RN [1]
RP SEQUENCE FROM N.A.
RA Yin Z.X., He J.G., Ye Q.Z., Wang S.P., Zhai Y.L.;
RT "Cloning and sequencing of hemoglobin beta gene of orange-spotted
RT grouper (Epinephelus coioides)."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY029506; AAK38736.1; -;
SQ SEQUENCE 147 AA; 16544 MW; EC389C1010ECDFEE CRC64;

Query Match 70.0%; Score 7; DB 13; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.29;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 VYPWTOR 9
Db 35 VYPWTOR 41

RESULT 95

ID P70073 PRELIMINARY; PRT; 148 AA.

AC P70073;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE BETA-GLOBIN.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA Yoshizaki G.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL; D88118; BAA13538.1; -;
DR EMBL; D88115; BAA13535.1; -;
DR EMBL; D88120; BAA13540.1; -;
DR HSSP; P56251; ISPG.
DR InterPro; IPR002337; Beta.haem.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PRINTS; PRO0814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
SQ SEQUENCE 148 AA; 16325 MW; A21F8802A9BB8FBA CRC64;

Query Match 70.0%; Score 7; DB 13; Length 148;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 VYPWTOR 9
Db 35 VYPWTOR 41

RESULT 96

ID 013140 PRELIMINARY; PRT; 148 AA.

AC 013140;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE BETA-GLOBIN.
GN NO.3 BETA.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA Miyata M.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Miyata M., Aoki T.;
RT "Head-to-Head linkage of carp alpha- and beta-globin genes.";
RL Biochim. Biophys. Acta 0:0-0(0).
RN [3]
RP SEQUENCE FROM N.A.
RA Miyata M., Hirono I., Aoki T.;

RT "Analysis of alpha-globin gene family of carp. I. alpha-globin gene structure of No.3, No.6, and No.7.";
 RL Nippon Suisan Gakkaishi 59:1077-1083(1993).
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: AB004740; BAA20516.1; -.
 DR HSSP: P56251; 1SPG.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 DR Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 SO SEQUENCE 148 AA; 16343 MW; 42D28816F9B6FEA3 CRC64;

Query Match 70.0%; Score 7; DB 13; Length 148;
 Best Local Similarity 100.0%; Pred. No. 0.29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 VYPWTOR 9
 DB 35 VYPWTOR 41

RESULT 97
 ID Q98851 PRELIMINARY; PRT; 148 AA.
 AC Q98851;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE BETA-GLOBIN.
 OS Cyprinus carpio (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Cyprinus.
 OX NCBI_TaxID=7962;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yoshizaki G.;
 RT "Cloning and sequencing of adult carp beta-globin family cDNA.";
 RL Submitted (SEP-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: D88116; BAA13536.1; -.
 DR HSSP: P56251; 1SPG.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 DR Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 SO SEQUENCE 148 AA; 16371 MW; 42CC68F8E9B6FEA3 CRC64;

Query Match 70.0%; Score 7; DB 13; Length 148;
 Best Local Similarity 100.0%; Pred. No. 0.29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 VYPWTOR 9
 DB 35 VYPWTOR 41

RESULT 98
 ID Q98852 PRELIMINARY; PRT; 148 AA.
 AC Q98852;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE BETA-GLOBIN.
 OS Cyprinus carpio (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 CC Cypriniformes; Cyprinidae; Cyprinus.
 OX NCBI_TaxID=7962;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yoshizaki G.;
 RT "Cloning and sequencing of adult carp beta-globin family cDNA.";
 RL Submitted (SEP-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: D88117; BAA13537.1; -.
 DR HSSP: P56251; 1SPG.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 DR Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 SO SEQUENCE 148 AA; 16397 MW; 03CC68F8E9B6FE2CF CRC64;

Query Match 70.0%; Score 7; DB 13; Length 148;
 Best Local Similarity 100.0%; Pred. No. 0.29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 VYPWTOR 9
 DB 35 VYPWTOR 41

RESULT 99
 ID Q98853 PRELIMINARY; PRT; 148 AA.
 AC Q98853;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE BETA-GLOBIN.
 OS Cyprinus carpio (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Cyprinus.
 OX NCBI_TaxID=7962;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yoshizaki G.;
 RT "Cloning and sequencing of adult carp beta-globin family cDNA.";
 RL Submitted (SEP-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR EMBL: D88119; BAA13539.1; -.
 DR HSSP: P56251; 1SPG.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 DR Erythrocyte; Heme; Oxygen transport; Respiratory protein.
 SO SEQUENCE 148 AA; 16482 MW; 03C8F098BD3E7CF CRC64;

Query Match 70.0%; Score 7; DB 13; Length 148;
 Best Local Similarity 100.0%; Pred. No. 0.29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 VYPWTOR 9
 DB 35 VYPWTOR 41

RESULT 100
 ID Q90485 PRELIMINARY; PRT; 148 AA.
 AC Q90485;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE BA2 GLOBIN.
GN BA2 OR BA2.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Danio.
OX NCBI_Taxid=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Zon L.;
RL Submitted (FEb-1996) to the EMBL/Genbank/DDbJ databases.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR EMBL; U50379; AAB05402.1; -.
DR HSSP; P56251; ISP6.
DR ZFIN; ZDB-GENE-990415-19; ba2.
DR InterPro; IPR002337; Beta_haem.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
KW Erythrocyte; Heme; Oxygen transport; Respiratory protein.
SQ SEQUENCE 148 AA; 16389 MW; BC358532B7EC144 CIRC64;

Query Match 70.0%; Score 7; DB 13; Length 148;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VYPWQR 9
|||
DB 35 VYPWQR 41

Search completed: July 1, 2002, 12:10:33
Job time: 221 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 1, 2002, 12:06:27 ; Search time 30.01 Seconds

(without alignments)
37.012 Million cell updates/sec

Title: US-09-147-490-1

Perfect score: 10

Sequence: 1 LVVYPWTRF 10

Scoring table:

OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 11073796 residues

Word size : 0

Total number of hits satisfying Chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	100.0	10	17	AA097348
2	10	100.0	10	18	AA030318
3	10	100.0	10	19	AA037247
4	10	100.0	10	6	AA050291
5	10	100.0	10	16	AA069602
6	10	100.0	10	22	AA007245
7	10	100.0	10	22	AA030074
8	10	100.0	10	22	AA002538
9	10	100.0	10	16	AA089261
10	10	100.0	10	16	AA089261
11	10	100.0	10	21	AA001752

12	10	100.0	124	22	AA029698	Novel human secret
13	10	100.0	127	22	AA013066	Human polypeptide
14	10	100.0	128	22	AA009585	Human polypeptide
15	10	100.0	137	22	AA030769	Novel human secret
16	10	100.0	140	22	AA079250	Human protein SEQ
17	10	100.0	141	18	AA030718	Haemoglobin beta(-
18	10	100.0	142	22	AA029784	Novel human secret
19	10	100.0	143	22	AA029796	Novel human secret
20	10	100.0	143	22	AA029798	Novel human secret
21	10	100.0	143	22	AA029847	Novel human secret
22	10	100.0	143	22	AA029890	Novel human secret
23	10	100.0	143	22	AA029920	Novel human secret
24	10	100.0	143	22	AA029929	Novel human secret
25	10	100.0	143	22	AA029955	Novel human secret
26	10	100.0	143	22	AA029961	Novel human secret
27	10	100.0	143	22	AA029977	Novel human secret
28	10	100.0	143	22	AA030020	Novel human secret
29	10	100.0	143	22	AA030022	Novel human secret
30	10	100.0	143	22	AA030024	Novel human secret
31	10	100.0	143	22	AA030028	Novel human secret
32	10	100.0	143	22	AA030030	Novel human secret
33	10	100.0	143	22	AA030083	Novel human secret
34	10	100.0	143	22	AA030099	Novel human secret
35	10	100.0	143	22	AA030132	Novel human secret
36	10	100.0	143	22	AA032926	Novel human secret
37	10	100.0	144	13	AA029611	Mutant human beta-
38	10	100.0	144	13	AA039726	HDA McKees Rock.
39	10	100.0	144	19	AA073382	Human haemoglobin
40	10	100.0	145	13	AA020303	Val(1) to Met, His
41	10	100.0	145	13	AA020305	Val(1) to Met, His
42	10	100.0	145	13	AA020306	Met(1), His(2) del
43	10	100.0	145	22	AA010346	Human polypeptide
44	10	100.0	146	9	AA081301	Mutant beta-globin
45	10	100.0	146	11	AA080815	des-Val beta globi
46	10	100.0	146	11	AA020302	Mutant "E11 (67) V
47	10	100.0	146	13	AA020304	"H01 Lys(144) to A
48	10	100.0	146	13	AA020307	Glu(3) beta-globin
49	10	100.0	146	13	AA020308	Gly(5) beta-globin
50	10	100.0	146	13	AA020310	Ala(5) beta-globin
51	10	100.0	146	13	AA020311	Glu(66) beta-globi
52	10	100.0	146	13	AA020312	Asp(68) beta-globi
53	10	100.0	146	13	AA020316	Thr(70) beta-globi
54	10	100.0	146	13	AA020317	Ser(70) beta-globi
55	10	100.0	146	13	AA021915	Cys(75) beta-globi
56	10	100.0	146	13	AA021916	Met(75) beta-globi
57	10	100.0	146	13	AA021917	Arg(76) beta-globi
58	10	100.0	146	13	AA021918	His(76) beta-globi
59	10	100.0	146	13	AA021919	Lys(76) beta-globi
60	10	100.0	146	13	AA021920	Met(1) beta-globin
61	10	100.0	146	13	AA021921	Leu(1) human beta-
62	10	100.0	146	13	AA021922	Leu(2) human beta-
63	10	100.0	146	13	AA021923	Tyr(2) human beta-
64	10	100.0	146	13	AA021924	Asp(2) human beta-
65	10	100.0	146	13	AA021925	Met(1), Leu(2) hum
66	10	100.0	146	13	AA021926	Met(1), Asp(2) hum
67	10	100.0	146	13	AA021927	Met(1), Tyr(2) hum
68	10	100.0	146	13	AA021928	Leu(1), Leu(2) hum
69	10	100.0	146	13	AA021929	Leu(1), Asp(2) hum
70	10	100.0	146	13	AA021930	Leu(1), Tyr(2) hum
71	10	100.0	146	13	AA021931	Mutant human beta-
72	10	100.0	146	13	AA021932	Mutant human beta-
73	10	100.0	146	13	AA021933	Agonist beta globi
74	10	100.0	146	13	AA021934	E90G beta globin.
75	10	100.0	146	13	AA021935	Yoshioka beta glo
76	10	100.0	146	13	AA021936	Kansas beta globin
77	10	100.0	146	13	AA021937	Beth israel beta g
78	10	100.0	146	13	AA021938	Root effect beta g
79	10	100.0	146	13	AA021939	Human beta Haemog
80	10	100.0	146	13	AA021940	
81	10	100.0	146	13	AA021941	
82	10	100.0	146	13	AA021942	
83	10	100.0	146	13	AA021943	
84	10	100.0	146	13	AA021944	

85	10	100.0	146	14	AAR39716	Human embryonic ep
86	10	100.0	146	14	AAR39717	Human fetal gamma
87	10	100.0	146	14	AAR39718	Human adult delta
88	10	100.0	146	14	AAR39720	Human beta alpha h
89	10	100.0	146	14	AAR39721	HbF Chico haemoglo
90	10	100.0	146	14	AAR39724	HbA Deer Lodge. H
91	10	100.0	146	14	AAR39725	HbA Aduzzzo. Homo
92	10	100.0	146	14	AAR39458	Des-Val beta globi
93	10	100.0	146	14	AAR42632	Natural beta-globi
94	10	100.0	146	15	AAR55132	Human beta haemogl
95	10	100.0	146	15	AAR44522	Adult human beta-g
96	10	100.0	146	15	AAR44523	Adult human beta-g
97	10	100.0	146	15	AAR44524	Adult human beta-g
98	10	100.0	146	15	AAR44525	Adult human beta-g
99	10	100.0	146	15	AAR44526	Adult human beta-g
100	10	100.0	146	15	AAR44527	Adult human beta-g

ALIGNMENTS

RESULT 1

AAR97348 standard; Protein; 10 AA.

AAR97348;

17-OCT-1996 (first entry)

Peptide fragment of haemoglobin B (Haemorphin 10).

haemoglobin; INPROL; stem cell proliferation; B lymphocytes;

B cells; chemotherapy; cancer; haematopoietic cells; marrow; blood;

myeloproliferative disease; autoimmune disease; adjuvant;

vaccination; immunodepression; gene therapy.

Homo sapiens.

WO9610634-A1.

11-APR-1996.

29-SEP-1995; 95WO-US12268.

28-SEP-1995; 95US-0535882.

30-SEP-1994; 94US-0316424.

(PRON-) PRO-NEURON INC.

Kozlov V, Tsyrlava I, Wolpe SD;

WPI; 1996-209356/21.

Inhibitors of stem cell proliferation comprising haemoglobin chains

useful in mammals, e.g. for protecting stem cells from antiviral

agents, treating cancer, and maintaining mammalian haematopoietic

stem cells ex vivo

Claim 17; Page 65; 10pp; English.

Compositions (INPROL) comprising a polypeptide selected from the

haemoglobin alpha, beta, gamma, delta, epsilon or zeta chains and a

carrier may be used to inhibit stem cell proliferation. INPROL can

also be used for stimulating the growth of B cells and can be used

with radio- or chemotherapy to treat cancer in mammals by

differentially protecting normal stem cells and not cancer cells

from such therapy. INPROL is also useful for maintaining mammalian

haematopoietic stem cells ex vivo (particularly bone marrow,

peripheral blood or cord blood cells); for the ex vivo expansion of

haematopoietic cells when used in combination with a stimulatory

cytokine. INPROL can also be used to treat myeloproliferative or

autoimmune disease. INPROL is also useful as an adjuvant in the

vaccination of mammals and can be used to treat a mammal with

CC immunodepression caused by stem cell proliferation. INPROL can also
CC be used in gene therapy. This peptide fragment of human haemoglobin
CC B corresponds to amino acids 32-41 of the mature protein given in
CC AAR97358.
SQ Sequence 10 AA:

Query Match 100.0%; Score 10; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPTQRF 10
DB 1 LVVYPTQRF 10

RESULT 2

AAW30318 standard; peptide; 10 AA.

AAW30318;

20-APR-1998 (first entry)

Peptide haemorphin 10 with opiate activity.

INPROL; stem cell; inhibition; stimulation; proliferation; myoglobin;

alpha chain; haemoglobin; radiotherapy; chemotherapy; cancer;

differential protection; stem cell hypoproliferation; aplastic anaemia;

stem cell exhaustion; haemorphin; opiate activity.

Synthetic.

Homo sapiens.

WO9736922-A1.

09-OCT-1997.

03-APR-1997; 97WO-US05601.

03-APR-1996; 96US-0627173.

(PRON-) PRO-NEURON INC.

Tsyrlava I, Wolpe SD;

WPI; 1997-503044/46.

Haemoglobin alpha chain derivatives - used to inhibit or stimulate

stem cell proliferation, for treatment of cancer, immune depression

etc

Claim 49; Page 117; 162pp; English.

The present peptide is derived from amino acids 32-41 of the beta

chain of adult human haemoglobin. The peptide has sequence similarity

and biological activity similar to other atypical opiate peptides. The

peptide can stimulate or inhibit stem cell proliferation, similar to

INPROL compounds. The peptide is used to inhibit stem cell proliferation,

particularly during radiotherapy or chemotherapy of cancer, but more

generally wherever a mammal is exposed to an agent, e.g. an antiviral,

that damages or destroys stem cells. It can also be used for differential

protection of normal stem cells, but not cancer cells, from chemotherapy

or radiation, particularly after normal stem cells have been induced to

proliferate by therapeutic treatment. The peptide can also be used for

control of stem cell hypoproliferation (e.g. aplastic anaemia), for

treating or preventing stem cell exhaustion (e.g. where caused by

acquired immune deficiency syndrome), and to treat or prevent

immunodeficiency. INPROL can also be used for treating pain in a mammal.

INPROL and related compounds reversibly inhibit or stimulate stem cells

depending on the dose, so allow precise control over cycling of these

cells.

XX Sequence 10 AA;

Query Match 100.0%; Score 10; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
| | | | | | | | | |
Db 1 lvvypwtgrf 10

RESULT 3

AAW37247
ID AAW37247 standard; peptide; 10 AA.

AC AAW37247;

DT 18-JUN-1998 (first entry)

DE Angiotensin IV activity exhibiting neuroactive peptide LVV-haemorphin-7.

XX Angiotensin IV; neuroactive; Alzheimer's disease; modulator; dementia;

KM neuronal development; vasoeffective; neuropathy; brain injury;

KW LVV-haemorphin-7.

OS Synthetic.

OS Macaca fascicularis.

XX MO9801465-A1.

XX 15-JAN-1998.

PF 09-JUL-1997; 97WO-AU00436.

XX 09-JUL-1996; 96AU-0000893.

PR (FLOR-) FLOREY INST EXPERIMENTAL PHYSIOLOGY.

XX WPI; 1998-100995/09.

DR Neuro-active peptide with activities of angiotensin IV and related

XX DNA - antagonists and oligo:nucleotide(s), useful for modulating

XX neuronal development and activity of motor and cholinergic neurons

PS Claim 1; Page 45; 65pp; English.

XX This LVV-haemorphin-7 is a neuroactive peptide with at least 1 of the

XX activities of angiotensin IV. This is an agonist of the angiotensin IV

XX receptor and is its endogenous ligand in the brain. It can modulate

XX learning or behaviour and has vasoeffective effects and can dilate cerebral

XX arteries, increase renal blood flow and stereotypy behaviour, facilitate

XX memory retrieval, induce neurite remodelling, and alleviate effects of

XX spinal cord injuries. This peptide and its antagonists are used to

XX modulate activity of motor, cholinergic neurons and neuronal development.

XX Specific applications are in treatment of dementia, Alzheimer's disease,

XX neurodegeneration (involving cholinergic, motor or sensory pathways),

XX sensory and motor peripheral neuropathy, brain injury and/or spinal cord

XX injury (caused by one or more of trauma, hypoxia and/or vascular

XX disease). Antibodies specific for the peptide can be used to determine

XX its amount of in tissues and tissue regions.

OY 1 LVVYPWTQRF 10
| | | | | | | | | |
Db 1 lvvypwtgrf 10

RESULT 4
AAP50291
ID AAP50291 standard; Protein; 74 AA.

AC AAP50291;

DT 30-NOV-1991 (first entry)

DE Sequence encoded by second exon of rabies glycoprotein gene.

XX Rabies vaccine; therapy; glycoprotein; antigen; diagnosis.

XX Rabies virus.

XX MO8501516-A.

PD 11-APR-1985.

PE 02-OCT-1984; 84WO-4000217.

XX 27-MAR-1984; 84FR-0004754.

PR 03-OCT-1984; 84FR-0015716.

PR 03-OCT-1983; 83FR-0015716.

XX (TRAN-) TRANSGENE SA.

PA (LATH/) LATHIE R.

XX Lathe R, Kieny MP, Lemoine Y, Loison G, Aigle M;

XX WPI; 1985-098845/16.

DR N-PSDB; AAN50333.

XX Vector for expressing rabies antigen - in eucaryotic cells,

XX useful for making vaccines and curative agents

XX Example; Fig 10; 62pp; French.

XX The inventors claim a vector for expressing a rabies antigen protein

XX in eucaryotic cells. After glycosylation with a yeast (specifically

XX at Asp residues 204 and 319), the recombinant antigen protein is

XX useful as a vaccine or curative agent. The coding sequence in the

XX vector can be followed by an intron (see AAN50333, N50334) or sites of

XX polyadenylation.

XX Sequence 74 AA;

QY 1 LVVYPWTQRF 10
| | | | | | | | | |
Db 2 lvvypwtgrf 11

RESULT 5
AAR69602
ID AAR69602 standard; Protein; 74 AA.

AC AAR69602;

DT 25-SEP-1995 (first entry)

DE Human beta-globin encoded by optimised exon 2.

XX Beta-globin; optimised codons; exon 2.

XX

OS Synthetic.
 XX
 PN WO9504744-A.
 XX
 PD 16-FEB-1995.
 XX
 XX 29-JUL-1994; 94WO-US08630.
 XX
 PR 11-AUG-1993; 93US-0105989.
 XX
 PA (DNXD-) DNK CORP.
 XX
 PI Khoury-christianson AM, Kumar R, Midha S, Paulhac C;
 PI Sharma A;
 DR WPI: 1995-090838/12.
 DR N-PSDB: AA083723.
 XX
 PT Production of human haemoglobin in transgenic pigs - by
 PT introducing gene constructs comprising human alpha and beta
 PT globin genes into pig ova, for an efficient source of haemoglobin
 PT for use in e.g. transfusions
 PS
 XX Example; Fig 39; 155pp; English.
 XX
 CC Human alpha-globin is expressed in transgenic pigs at higher levels
 CC than human beta-globin. One approach to increasing the level of
 CC expressed beta-globin is to engineer the human beta-globin gene
 CC from the promoter region through the coding sequence and into the
 CC polyA site and 3' UTR to be similar to pig beta-globin gene, but
 CC without altering the AA sequence from that of authentic wt human
 CC beta-globin. PCR was used to optimise human beta-globin gene for
 CC porcine expression. Equivalent fragments of the human and pig beta-
 CC globin coding sequences in exons 1, 2 are 3 are depicted in
 CC AA083716/083719, AA083717/083720 and AA083718/083721, respectively.
 CC These pairs of sequences may be compared for differences. Optimised
 CC human beta-globin coding sequences for exons 1, 2 and 3 are depicted in
 CC AA083722, AA083723 and AA083724, respectively. These sequences may be
 CC compared with AA083716, AA083717 and AA083718 respectively. The AA
 CC sequences encoded by the optimised human beta-globin coding sequences
 CC are given in AAR69601, AAR69602, AAR69603.
 XX
 SO Sequence 74 AA;

Query Match 100.0%; Score 10; DB 16; Length 74;
 Best Local Similarity 100.0%; Pred. No. 0.0001;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 |||||||||
 DB 2 LVVYPWTGRF 11

RESULT 6
 AA007245
 ID AA007245 standard; Protein; 86 AA.
 XX
 AC AA007245;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 21137.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200164835-A2.
 XX

PD 07-SEP-2001.
 XX
 XX 26-FEB-2001; 2001WO-US04927.
 XX
 PR 28-FEB-2000; 2000US-0515126.
 XX
 PR 18-MAY-2000; 2000US-0577409.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YF, Liu C, Drmanac RT;
 DR WPI: 2001-514838/56.
 DR N-PSDB: AA187176.
 XX
 PT Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -
 XX
 XX Claim 20; SEQ ID NO 21137; 1399pp + Sequence Listing; English.
 PS
 XX The invention relates to human polynucleotides (AA179941-AA193841) and
 XX the encoded proteins (AA000010-AA013910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activating
 CC activity/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SO Sequence 86 AA;

Query Match 100.0%; Score 10; DB 22; Length 86;
 Best Local Similarity 100.0%; Pred. No. 0.00012;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 |||||||||
 DB 33 LVVYPWTGRF 48

RESULT 7
 AA030074
 ID AA030074 standard; Protein; 104 AA.
 XX
 AC AA030074;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secreted protein #565.
 XX
 KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200179449-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US08656.
 XX
 PR 18-APR-2000; 2000US-0552929.
 PR 26-JAN-2001; 2001US-0770160.
 XX
 PA (HYSE-) HYSEQ INC.
 XX

XX Tang YT, Liu C, Drmanac RT;
 XX WPI: 2001-611725/70.
 DR Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy -
 XX
 PS Claim 20: Page 234; 765pp; English.
 XX The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemias. AA029510-AAU33304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.
 XX
 SQ Sequence 104 AA;
 Query Match 100.0%; Score 10; DB 22; Length 104;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVVYPWTFQRF 10
 |||||
 Db 33 LVVYPWTFGRF 42
 RESULT 8
 AA002538
 ID AA002538 standard; Protein; 110 AA.
 XX
 AC AA002538;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 16430.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200164835-A2.
 XX
 PD 07-SEP-2001.
 XX
 PF 26-FEB-2001; 2001WO-US04927.
 XX
 PR 28-FEB-2000; 2000US-0515126.
 PR 18-MAY-2000; 2000US-0577409.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI: 2001-514838/56.
 DR N-PSDB; AAI82469.
 XX

PT Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -
 XX
 PS Claim 20; SEQ ID NO 16430; 1399pp + Sequence Listing; English.
 XX The invention relates to human polynucleotides (AA179941-AA193841) and
 CC the encoded proteins (AA000010-AA013910) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 110 AA;
 Query Match 100.0%; Score 10; DB 22; Length 110;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVVYPWTFQRF 10
 |||||
 Db 17 LVVYPWTFGRF 26
 RESULT 9
 AAR89262
 ID AAR89262 standard; peptide; 112 AA.
 XX
 AC AAR89262;
 XX
 DT 04-MAR-1996 (first entry)
 XX
 DE Human beta-globin mutant Val90, Met91, Ser93, Glu94.
 XX
 KW Human beta-globin; mutant Val90, Met91, Ser93, Glu94; hypoxic cells;
 KW increased oxygenation; radiation therapy; vascular diseases.
 XX
 OS Homo sapiens.
 XX
 PN US5428007-A.
 XX
 PD 27-JUN-1995.
 XX
 PF 06-OCT-1989; 89US-0417949.
 XX
 PR 06-OCT-1989; 89US-0417949.
 PR 09-OCT-1992; 92US-0959286.
 PR 28-APR-1994; 94US-0235118.
 XX
 PA (UYVA) UNIV YALE.
 XX
 PI Baserga SJ, Fischer JT;
 XX
 DR WPI: 1995-240064/31.
 XX
 PT Increasing tissue oxygen in hypoxic cells - by administering a pure
 PT mutant alpha or beta haemoglobin having a low oxygen affinity.
 XX
 PS Example 3; Columns 5-6; 10pp; English.
 XX
 CC AAR89262 is the human beta-globin mutant Val90, Met91, Ser93, Glu94.
 CC The mutant globin can be used to increase tissue oxygenation in
 CC hypoxic cells, to increase oxygenation in tumours to enhance the
 CC effects of radiation therapy or as a blood replacement or

CC treatment in vascular diseases.
XX
SQ Sequence 112 AA;

Query Match 100.0%; Score 10; DB 16; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
| | | | | | | | | |
DB 32 LVVYPWTORE 41

RESULT 10
AAR89261
ID AAR89261 standard; peptide; 112 AA.

AC AAR89261;

DT 04-MAR-1996 (first entry)

DE Human beta-globin mutant Gln/Lys90 and Aspl08.

KW Human beta-globin; mutant Gln/Lys90 and Aspl08; hypoxic cells;
increased oxygenation; radiation therapy; vascular diseases.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Misc-difference 90 /label= Gln, Lys

PN US5428007-A.

PD 27-JUN-1995.

PF 06-OCT-1989; 89US-0417949.

PR 06-OCT-1989; 89US-0417949.

PR 09-OCT-1992; 92US-0959286.

PR 28-APR-1994; 94US-0235118.

PA (UYVA) UNITV YALE.

PI Baserga SJ, Fischer JJ;

DR WPI; 1995-240064/31.

XX Increasing tissue oxygen in hypoxic cells - by administering a pure

PT mutant alpha or beta haemoglobin having a low oxygen affinity.

PS Example 3; Columns 5-6; 10pp; English.

CC AAR89261 is the human beta-globin mutant Gln/Lys90 and Aspl08.

CC The mutant globin can be used to increase tissue oxygenation in

CC hypoxic cells, to increase oxygenation in tumours to enhance the

CC effects of radiation therapy or as a blood replacement or

CC treatment in vascular diseases.

SQ Sequence 112 AA;

OY 1 LVVYPWTORE 10
| | | | | | | | | |
DB 32 LVVYPWTORE 41

RESULT 11

AAG01752
ID AAG01752 standard; Protein; 121 AA.

AC AAG01752;

DT 06-OCT-2000 (first entry)

DE Human secreted protein, SEQ ID NO: 5833.

KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;

KW gene therapy; chromosome mapping.

OS Homo sapiens.

PN EP1033401-A2.

PD 06-SEP-2000.

PF 21-FEB-2000; 2000EP-0200610.

PR 26-FEB-1999; 99US-0122487.

XX (GEST) GENSET.

PI Dumas Milne Edwards J, Duclert A, Giordano J;

DR WPI; 2000-500381/45.

DR N-PSDB; AAC01758.

PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for

PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for

PT diagnostic, forensic, gene therapy and chromosome mapping procedures -

PS Claim 13; SEQ ID 5833; 71pp + CD-ROM; English.

CC The present sequence is a polypeptide encoded by one of a large number

CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs

CC were prepared from total human RNAs or polyA+ RNAs derived from 30

CC different tissues. EST sequences usually correspond mainly to the 3'

CC untranslated region (UTR) of the mRNA because they are often obtained

CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for

CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in

CC those cases where longer cDNA sequences have been obtained, the full 5'

CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'

CC ends and can therefore be used to obtain full length cDNAs and genomic

CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and

CC chromosome mapping procedures. They are used to obtain upstream

CC regulatory sequences and to design expression and secretion vectors.

SQ Sequence 121 AA;

OY 1 LVVYPWTORE 10
| | | | | | | | | |
DB 33 LVVYPWTORE 42

RESULT 12
AAU29698

ID AAU29698 standard; Protein; 124 AA.

AC AAU29698;

DT 18-DEC-2001 (first entry)

DE Novel human secreted protein #189.

KW Human; vaccination; gene therapy; nutritional supplement;

KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;

KW Immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX Homo sapiens.
 OS
 PN WO200179449-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US08656.
 XX
 PR 18-APR-2000; 2000US-0552929.
 PR 26-JAN-2001; 2001US-0770160.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-611725/70.
 XX
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy -
 XX
 PS Claim 20: Page 181; 765pp; English.
 XX
 CC The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemias. AA029510-AA03304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.
 XX
 SQ Sequence 124 AA;
 XX
 QY 1 LVVYPWTFQRF 10
 Db 39 LVVYPWTFQRF 48
 XX
 RESULT 13
 AA013066
 ID AA013066 standard; Protein; 127 AA.
 XX
 AC AA013066;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 26958.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200164835-A2.
 XX

PD 07-SEP-2001.
 XX
 PF 26-FEB-2001; 2001WO-US04927.
 XX
 PR 28-FEB-2000; 2000US-0515126.
 PR 18-MAY-2000; 2000US-0577409.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-514838/56.
 DR N-PSDB; AA192997.
 XX
 PT Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -
 XX
 PS Claim 20; SEQ ID NO 26958; 139pp + Sequence Listing; English.
 XX
 CC The invention relates to human polynucleotides (AA179941-AA193841) and
 CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at http://wipo.int/pub/published_pcl_sequences.
 XX
 SQ Sequence 127 AA;
 XX
 QY 1 LVVYPWTFQRF 10
 Db 39 LVVYPWTFQRF 48
 XX
 RESULT 14
 AA009585
 ID AA009585 standard; Protein; 128 AA.
 XX
 AC AA009585;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 23477.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200164835-A2.
 XX
 PD 07-SEP-2001.
 XX
 DE 26-FEB-2001; 2001WO-US04927.
 XX
 PF 28-FEB-2000; 2000US-0515126.
 PR 18-MAY-2000; 2000US-0577409.
 XX

PA (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI: 2001-514838/56.
DR N-PSDB; AA189516.
XX
XX Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders.
XX
PS Claim 20: SEQ ID NO 23477; 1399pp + Sequence Listing; English.
XX
XX The invention relates to human polynucleotides (AA179941-AA193841) and
CC the encoded proteins (AA000010-AA03910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activity/inhibit activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 128 AA:

Query Match 100.0%; Score 10; DB 22; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LVVYPWTQRF 10
|||
DB 39 LVVYPWTQRF 48

RESULT 15
AAU30769
ID AAU30769 standard; Protein: 137 AA.
XX
XX AAU30769;
AC
XX
XX 18-DEC-2001 (first entry)
DT
XX
DE Novel human secreted protein #1260.
XX
XX Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
XX Homo sapiens.
OS
XX
XX WO200179449-A2.
PN
XX
XX 25-OCT-2001.
PD
XX
XX 16-APR-2001; 2001WO-US08656.
PF
XX
XX 18-APR-2000; 2000US-0552929.
PR
XX
XX 26-JAN-2001; 2001US-0770160.
PR
XX
XX (HYSE-) HYSEQ INC.
PA
XX
XX Tang YT, Liu C, Drmanac RT;
PI
XX
XX WPI: 2001-611725/70.
DR
XX
XX Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy.

XX
XX Claim 20; Page 342; 765pp; English.
XX
XX The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising
CC the nucleic acids encoding the polypeptides and cells genetically
CC engineered to express them are also useful for producing the proteins.
CC The proteins are useful in genetic vaccination, testing and
CC therapy, and can be used as nutritional supplements. They may be used to
CC increase stem cell proliferation; to regulate haematopoiesis; and in
CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
CC immune suppression of leukaemias. AAU29510-AAU3304 represent the amino acid
CC sequences of novel human secreted proteins of the invention.
XX
SQ Sequence 137 AA:

Query Match 100.0%; Score 10; DB 22; Length 137;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LVVYPWTQRF 10
|||
DB 51 LVVYPWTQRF 60

RESULT 16
AAM79250
ID AAM79250 standard; Protein: 140 AA.
XX
XX AAM79250;
AC
XX
XX 06-NOV-2001 (first entry)
DT
XX
DE Human protein SEQ ID NO 1912.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
XX Homo sapiens.
OS
XX
XX WO200157190-A2.
PN
XX
XX 09-AUG-2001.
PD
XX
XX 05-FEB-2001; 2001WO-US04098.
PF
XX
XX 03-FEB-2000; 2000US-0496914.
PR
XX
XX 27-APR-2000; 2000US-0560875.
PR
XX
XX 20-JUN-2000; 2000US-0598075.
PR
XX
XX 19-JUL-2000; 2000US-0620325.
PR
XX
XX 01-SEP-2000; 2000US-0654936.
PR
XX
XX 15-SEP-2000; 2000US-0663561.
PR
XX
XX 20-OCT-2000; 2000US-0693325.
PR
XX
XX 30-NOV-2000; 2000US-0728422.
PR
XX
XX (HYSE-) HYSEQ INC.
PA
XX
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX WPI: 2001-476283/51.
DR
XX
XX N-PSDB; AAK52383.

XX Nucleic acids encoding polypeptides with cytokine-like activities.
 PT useful in diagnosis and gene therapy -
 PS
 PS Claim 20. Page 4310-4311: 6221pp; English.
 XX
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAW80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activity/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAM80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.
 CC
 SQ Sequence 140 AA:
 QY 1 LVVYPWTQRF 10
 100.0%; Score 10; DB 22; Length 140;
 Best Local Similarity 100.0%; Pred. No. 0.00018;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 33 lvvypwtgrf 42
 RESULT 17
 AAM30718
 ID AAM30718 standard; Protein; 141 AA.
 XX
 AC AAM30718;
 XX
 DT 14-JAN-1998 (first entry)
 XX
 DE Haemoglobin beta(-D) variant chain.
 XX
 KW Haemoglobin; Hb; alpha: beta; wild type; variant; haem loss;
 KW stability; red blood cell substitute; volume expander; gas content;
 KW drug delivery; imaging; scavenger; haemolytic anaemia; porphyria;
 KW haemochromatosis.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9715591-A1.
 XX
 PD 01-MAY-1997.
 XX
 PF 23-OCT-1996; 96WO-US16934.
 XX
 PR 23-OCT-1995; 95US-0006020.
 PR 04-DEC-1995; 95US-0566780.
 XX
 PA (R1CV) UNIV RICE.
 XX
 PI Hargrove MS, Olson JS, Whitaker TL;
 DR WPI; 1997-258953/23.
 XX
 PT Reducing haem loss in haemoglobin by specific amino acid alterations
 PT - to improve stability and recombinant expression, useful as blood
 PT substitutes, scavengers of excess haem etc.
 XX
 PS Claim 6; Page -: 30pp; English.
 XX
 CC This is a human haemoglobin (Hb) beta chain variant, designated

CC beta(-D), created by deletion of residues Thr50-Pro-Asp-Ala-Val54 from
 CC the native sequence (see AAM30717). Hb variants (AAM30718-30 and
 CC AAM30733-36) were used to create single and double mutant Hb hybrids in
 CC combination with wild type alpha (AAM30716) and beta chains. Novel mutant
 CC Hbs where the substitution is not specified are indicated in AAM30731-32.
 CC Other Hb mutants are known. The rate of haem loss in the Hb mutants was
 CC determined by assays for ligand binding, autooxidation rates and haem
 CC dissociation rates. In particular, haem loss in Hb is reduced by altering
 CC the sequence of a Hb subunit with one of the following mutations: (a)
 CC addition of a D-helix region to an alpha subunit; (b) altering
 CC Leu28(B10), Met32(B13), Thr38(C4), Phe41(C7), Phe42(CD1), Ser44(CD3),
 CC Phe45(CD4), the entire D helix, His63(E7), Gly64(E8), Lys66(E10),
 CC Val67(E11), Ala70(E14), Leu88(F4), Leu91(F7), His92(F8), Leu96(FG3),
 CC Val98(FG5), Asn102(G4), Phe103(G5), Leu110(G12), Gly136(H14),
 CC Val137(H15) or Leu141(H19) in the beta subunit; and (c) altering
 CC Leu29(B10), Leu31(B13), Thr39(C4), Tyr42(C7), Phe43(CD1), His45(CD3),
 CC Phe46(CD4), His58(E7), Glu59(E8), Lys61(E10), Val62(E11), Ala65(E14),
 CC Leu83(F4), Leu86(F7), His87(F8), Leu91(FG3), Val93(FG5), Asn97(G4),
 CC Phe98(G5), Leu101(G8), Leu102(G12), Ser131(H14), Val132(H15), or
 CC Leu136(H19) in the alpha subunit. The mutant Hb are used as red blood
 CC cell substitutes or volume expanders; as reference solutions for
 CC analytical instruments; as reagents; to control gas content of cell
 CC cultures (delivery or removal of oxygen); for drug delivery and imaging;
 CC to remove/deliver nitric oxide or non-oxygen ligands and to scavenge
 CC excess haem (e.g. for treatment of haemolytic anaemia, porphyria or
 CC haemochromatosis).
 CC
 SQ Sequence 141 AA:
 QY 1 LVVYPWTQRF 10
 100.0%; Score 10; DB 18; Length 141;
 Best Local Similarity 100.0%; Pred. No. 0.00018;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 32 lvvypwtgrf 41
 RESULT 18
 AAU29784
 ID AAU29784 standard; Protein; 142 AA.
 XX
 AC AAU29784;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secreted protein #275.
 XX
 KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; hematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 OS
 PN WO200179449-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US08656.
 XX
 PR 18-APR-2000; 2000US-0552929.
 PR 26-JAN-2001; 2001US-0770160.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 DR WPI; 2001-611725/70.
 XX
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy -
 XX

PS Claim 20; Page 194; 765pp; English.
XX The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising
CC the nucleic acids encoding the polypeptides and cells genetically
CC engineered to express them are also useful for producing the proteins.
CC The proteins are useful in genetic vaccination, testing and
CC therapy, and can be used as nutritional supplements. They may be used to
CC increase stem cell proliferation; to regulate haematopoiesis; and in
CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
CC immune suppression and/or stimulation; as anti-inflammatory agents; and
CC in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid
CC sequences of novel human secreted proteins of the invention.
XX
SQ Sequence 142 AA:

Query Match 100.0%; Score 10; DB 22; Length 142;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPMQRF 10
| | | | | | | | | |
Db 28 LVVYPMQRF 37

RESULT 19
AAU29796
ID AAU29796 standard; Protein: 143 AA.
XX
AC AAU29796;
XX
DT 18-DEC-2001 (first entry)
XX
DE Novel human secreted protein #287.
XX
KW Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200179449-A2.
XX
PD 25-OCT-2001.
XX
PF 16-APR-2001; 2001WO-US08656.
XX
PR 18-APR-2000; 2000US-0552929.
PR 26-JAN-2001; 2001US-0770160.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI: 2001-611725/70.
XX
PT Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy -
XX
PS Claim 20; Page 195; 765pp; English.
XX
CC The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising
CC the nucleic acids encoding the polypeptides and cells genetically
CC engineered to express them are also useful for producing the proteins.
CC The proteins are useful in genetic vaccination, testing and
CC therapy, and can be used as nutritional supplements. They may be used to

CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising
CC the nucleic acids encoding the polypeptides and cells genetically
CC engineered to express them are also useful for producing the proteins.
CC The proteins are useful in genetic vaccination, testing and
CC therapy, and can be used as nutritional supplements. They may be used to
CC increase stem cell proliferation; to regulate haematopoiesis; and in
CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
CC immune suppression and/or stimulation; as anti-inflammatory agents; and
CC in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid
CC sequences of novel human secreted proteins of the invention.
XX
SQ Sequence 143 AA:

Query Match 100.0%; Score 10; DB 22; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPMQRF 10
| | | | | | | | | |
Db 29 LVVYPMQRF 38

RESULT 20
AAU29798
ID AAU29798 standard; Protein: 143 AA.
XX
AC AAU29798;
XX
DT 18-DEC-2001 (first entry)
XX
DE Novel human secreted protein #289.
XX
KW Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200179449-A2.
XX
PD 25-OCT-2001.
XX
PF 16-APR-2001; 2001WO-US08656.
XX
PR 18-APR-2000; 2000US-0552929.
PR 26-JAN-2001; 2001US-0770160.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI: 2001-611725/70.
XX
PT Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy -
XX
PS Claim 20; Page 195; 765pp; English.
XX
CC The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising
CC the nucleic acids encoding the polypeptides and cells genetically
CC engineered to express them are also useful for producing the proteins.
CC The proteins are useful in genetic vaccination, testing and
CC therapy, and can be used as nutritional supplements. They may be used to

CC increase stem cell proliferation; to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.
 XX

SO Sequence 143 AA;

Query Match 100.0%; Score 10; DB 22; Length 143;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFQRF 10
 |||||
 DB 29 LVVYPWTFQRF 38

RESULT 21

ID AAU29847 standard; protein; 143 AA.

AC AAU29847;

DT 18-DEC-2001 (first entry)

DE Novel human secreted protein #338.

KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

OS Homo sapiens.

PN WO200179449-A2.

PD 25-OCT-2001.

PF 16-APR-2001; 2001WO-US08656.

PR 18-APR-2000; 2000US-0552929.

PR 26-JAN-2001; 2001US-0770160.

XX (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT;

DR WPI; 2001-611725/70.

PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy -

PS Claim 20; Page 201; 765pp; English.

CC The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.
 XX

SO Sequence 143 AA;

Query Match 100.0%; Score 10; DB 22; Length 143;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFQRF 10
 |||||
 DB 29 LVVYPWTFQRF 38

RESULT 22

ID AAU29890 standard; protein; 143 AA.

AC AAU29890;

DT 18-DEC-2001 (first entry)

DE Novel human secreted protein #381.

KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

OS Homo sapiens.

PN WO200179449-A2.

PD 25-OCT-2001.

PF 16-APR-2001; 2001WO-US08656.

PR 18-APR-2000; 2000US-0552929.

PR 26-JAN-2001; 2001US-0770160.

XX (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT;

DR WPI; 2001-611725/70.

PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy -

PS Claim 20; Page 207; 765pp; English.

CC The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.
 XX

SO Sequence 143 AA;

Query Match 100.0%; Score 10; DB 22; Length 143;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFQRF 10

Db 29 lvvypwtqrf 38

RESULT 23

AAU29920 standard; Protein; 143 AA.

AC AAU29920;

DT 18-DEC-2001 (first entry)

DE Novel human secreted protein #411.

KW Human: vaccination; gene therapy; nutritional supplement;

KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;

KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

OS Homo sapiens.

PN WO200179449-A2.

PD 25-OCT-2001.

PF 16-APR-2001; 2001WO-US08656.

PR 18-APR-2000; 2000US-0552929.

PR 26-JAN-2001; 2001US-0770160.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT;

DR WPI: 2001-611725/70.

PT Nucleic acids encoding a range of human polypeptides, useful in genetic

PS vaccination, testing and therapy -

XX Claim 20; Page 210; 765pp; English.

CC The invention relates to novel human secreted polypeptides. The

CC polypeptides and antibodies to the polypeptides are useful for

CC determining the presence of or predisposition to a disease associated

CC with altered levels of polypeptide. The polypeptides are also useful for

CC identifying agents (agonists and antagonists) that bind to them. Cells

CC expressing the proteins are useful for identifying a therapeutic agent

CC for use in treatment of a pathology related to aberrant expression or

CC physiological interactions of the polypeptide. Vectors comprising

CC the nucleic acids encoding the polypeptides and cells genetically

CC engineered to express them are also useful for producing the proteins.

CC The proteins are useful in genetic vaccination, testing and

CC therapy, and can be used as nutritional supplements. They may be used to

CC increase stem cell proliferation; to regulate haematopoiesis; and in

CC bone, cartilage, tendon and/or nerve tissue growth or regeneration.

CC Immune suppression and/or stimulation; as anti-inflammatory agents; and

CC in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid

CC sequences of novel human secreted proteins of the invention.

SO Sequence 143 AA;

Query Match 100.0%; Score 10; DB 22; Length 143;

Best Local Similarity 100.0%; Pred. No. 0.00019;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPTQRF 10

DB 29 LVVYPTQRF 38

RESULT 24

AAU29929 standard; Protein; 143 AA.

XX

AC AAU29929;

DT 18-DEC-2001 (first entry)

DE Novel human secreted protein #420.

KW Human: vaccination; gene therapy; nutritional supplement;

KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;

KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

OS Homo sapiens.

PN WO200179449-A2.

PD 25-OCT-2001.

PF 16-APR-2001; 2001WO-US08656.

PR 18-APR-2000; 2000US-0552929.

PR 26-JAN-2001; 2001US-0770160.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT;

DR WPI: 2001-611725/70.

PT Nucleic acids encoding a range of human polypeptides, useful in genetic

PS vaccination, testing and therapy -

XX Claim 20; Page 211; 765pp; English.

CC The invention relates to novel human secreted polypeptides. The

CC polypeptides and antibodies to the polypeptides are useful for

CC determining the presence of or predisposition to a disease associated

CC with altered levels of polypeptide. The polypeptides are also useful for

CC identifying agents (agonists and antagonists) that bind to them. Cells

CC expressing the proteins are useful for identifying a therapeutic agent

CC for use in treatment of a pathology related to aberrant expression or

CC physiological interactions of the polypeptide. Vectors comprising

CC the nucleic acids encoding the polypeptides and cells genetically

CC engineered to express them are also useful for producing the proteins.

CC The proteins are useful in genetic vaccination, testing and

CC therapy, and can be used as nutritional supplements. They may be used to

CC increase stem cell proliferation; to regulate haematopoiesis; and in

CC bone, cartilage, tendon and/or nerve tissue growth or regeneration.

CC Immune suppression and/or stimulation; as anti-inflammatory agents; and

CC in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid

CC sequences of novel human secreted proteins of the invention.

SO Sequence 143 AA;

Query Match 100.0%; Score 10; DB 22; Length 143;

Best Local Similarity 100.0%; Pred. No. 0.00019;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPTQRF 10

DB 29 LVVYPTQRF 38

RESULT 25

AAU29955 standard; Protein; 143 AA.

AC AAU29955;

DT 18-DEC-2001 (first entry)

DE Novel human secreted protein #446.

KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200179449-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US08656.
 XX
 PR 18-APR-2000; 2000US-0552929.
 PR 26-JAN-2001; 2001US-0770160.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-611725/70.
 XX
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy -
 XX
 PS Claim 20; Page 213; 765pp; English.
 XX
 CC The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.
 XX
 SQ Sequence 143 AA;
 XX

Query Match 100.0%; Score 10; DB 22; Length 143;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
 |||||
 Db 29 LVVYPWTQRF 38

RESULT 26
 AAU29961
 ID AAU29961 standard; Protein; 143 AA.
 XX
 AC AAU29961;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secreted protein #452.
 XX
 KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200179449-A2.

XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US08656.
 XX
 PR 18-APR-2000; 2000US-0552929.
 PR 26-JAN-2001; 2001US-0770160.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-611725/70.
 XX
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy -
 XX
 PS Claim 20; Page 214; 765pp; English.
 XX
 CC The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.
 XX
 SQ Sequence 143 AA;
 XX

Query Match 100.0%; Score 10; DB 22; Length 143;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
 |||||
 Db 29 LVVYPWTQRF 38

RESULT 27
 AAU29977
 ID AAU29977 standard; Protein; 143 AA.
 XX
 AC AAU29977;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secreted protein #468.
 XX
 KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200179449-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US08656.
 XX
 PR 18-APR-2000; 2000US-0552929.
 PR 26-JAN-2001; 2001US-0770160.

xx (HYSE-) HYSEQ INC.
xx
xx Tang YT, Liu C, Drmanac RT;
xx
xx WPI: 2001-611725/70.
xx
xx Nucleic acids encoding a range of human polypeptides, useful in genetic
xx vaccination, testing and therapy -
xx
xx Claim 20: Page 216; 765pp; English.
xx
xx The invention relates to novel human secreted polypeptides. The
xx polypeptides and antibodies to the polypeptides are useful for
xx determining the presence of or predisposition to a disease associated
xx with altered levels of polypeptide. The polypeptides are also useful for
xx identifying agents (agonists and antagonists) that bind to them. Cells
xx expressing the proteins are useful for identifying a therapeutic agent
xx for use in treatment of a pathology related to aberrant expression or
xx physiological interactions of the polypeptide. Vectors comprising
xx the nucleic acids encoding the polypeptides and cells genetically
xx engineered to express them are also useful for producing the proteins.
xx The proteins are useful in genetic vaccination, testing and
xx therapy, and can be used as nutritional supplements. They may be used to
xx increase stem cell proliferation; to regulate haematopoiesis; and in
xx bone, cartilage, tendon and/or nerve tissue growth or regeneration;
xx immune suppression and/or stimulation; as anti-inflammatory agents; and
xx in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid
xx sequences of novel human secreted proteins of the invention.
xx
xx Sequence 143 AA:
xx
xx

Query Match 100.0%; Score 10; DB 22; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORF 10
| | | | | | | | | |
DB 29 LVVYPWTORF 38

RESULT 28

AAU30020
ID AAU30020 standard; Protein: 143 AA.

AC AAU30020;

DT 18-DEC-2001 (first entry)

DE Novel human secreted protein #511.

KW Human: vaccination; gene therapy; nutritional supplement;

KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;

KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

OS Homo sapiens.

PN WO200179449-A2.

PD 25-OCT-2001.

PF 16-APR-2001; 2001WO-US08656.

PR 18-APR-2000; 2000US-0552929.

PR 26-JAN-2001; 2001US-0770160.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT;
xx WPI: 2001-611725/70.
xx

PT Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy -
xx
xx Claim 20: Page 221; 765pp; English.
xx
xx

xx The invention relates to novel human secreted polypeptides. The
xx polypeptides and antibodies to the polypeptides are useful for
xx determining the presence of or predisposition to a disease associated
xx with altered levels of polypeptide. The polypeptides are also useful for
xx identifying agents (agonists and antagonists) that bind to them. Cells
xx expressing the proteins are useful for identifying a therapeutic agent
xx for use in treatment of a pathology related to aberrant expression or
xx physiological interactions of the polypeptide. Vectors comprising
xx the nucleic acids encoding the polypeptides and cells genetically
xx engineered to express them are also useful for producing the proteins.
xx The proteins are useful in genetic vaccination, testing and
xx therapy, and can be used as nutritional supplements. They may be used to
xx increase stem cell proliferation; to regulate haematopoiesis; and in
xx bone, cartilage, tendon and/or nerve tissue growth or regeneration;
xx immune suppression and/or stimulation; as anti-inflammatory agents; and
xx in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid
xx sequences of novel human secreted proteins of the invention.
xx
xx Sequence 143 AA:
xx
xx

Query Match 100.0%; Score 10; DB 22; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORF 10
| | | | | | | | | |
DB 29 LVVYPWTORF 38

RESULT 29

AAU30022
ID AAU30022 standard; Protein: 143 AA.

AC AAU30022;

DT 18-DEC-2001 (first entry)

DE Novel human secreted protein #513.

KW Human: vaccination; gene therapy; nutritional supplement;

KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;

KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

OS Homo sapiens.

PN WO200179449-A2.

PD 25-OCT-2001.

PF 16-APR-2001; 2001WO-US08656.

PR 18-APR-2000; 2000US-0552929.

PR 26-JAN-2001; 2001US-0770160.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT;
xx WPI: 2001-611725/70.
xx

PT Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy -
xx
xx Claim 20: Page 222; 765pp; English.

xx The invention relates to novel human secreted polypeptides. The
xx polypeptides and antibodies to the polypeptides are useful for

determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention.

Sequence 143 AA:

Query Match 100.0%; Score 10; DB 22; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFQRF 10
|||||
DB 29 LVVYPWTFGRF 38

RESULT 30
AAU30024
ID AAU30024 standard; Protein; 143 AA.
XX
AC AAU30024;
XX
DT 18-DEC-2001 (first entry)
XX
DE Novel human secreted protein #515.
XX
KW Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200179449-A2.
XX
PD 25-OCT-2001.
XX
PF 16-APR-2001; 2001WO-US08656.
XX
PR 18-APR-2000; 2000US-0552929.
PR 26-JAN-2001; 2001US-0770160.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YF, Liu C, Drmanac RT;
XX
DR WPI; 2001-611725/70.
XX
PT Nucleic acids encoding a range of human polypeptides, useful in genetic
XX vaccination, testing and therapy -
XX
PS Claim 20; Page 222; 765pp; English.
XX
XX The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising
CC the nucleic acids encoding the polypeptides and cells genetically

engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention.

Sequence 143 AA:

Query Match 100.0%; Score 10; DB 22; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFQRF 10
|||||
DB 29 LVVYPWTFGRF 38

RESULT 31
AAU30028
ID AAU30028 standard; Protein; 143 AA.
XX
AC AAU30028;
XX
DT 18-DEC-2001 (first entry)
XX
DE Novel human secreted protein #519.
XX
KW Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200179449-A2.
XX
PD 25-OCT-2001.
XX
PF 16-APR-2001; 2001WO-US08656.
XX
PR 18-APR-2000; 2000US-0552929.
PR 26-JAN-2001; 2001US-0770160.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YF, Liu C, Drmanac RT;
XX
DR WPI; 2001-611725/70.
XX
PT Nucleic acids encoding a range of human polypeptides, useful in genetic
XX vaccination, testing and therapy -
XX
PS Claim 20; Page 222; 765pp; English.
XX
XX The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising
CC the nucleic acids encoding the polypeptides and cells genetically
CC engineered to express them are also useful for producing the proteins.
CC The proteins are useful in genetic vaccination, testing and
CC therapy, and can be used as nutritional supplements. They may be used to
CC increase stem cell proliferation; to regulate haematopoiesis; and in
CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
CC immune suppression and/or stimulation; as anti-inflammatory agents; and
CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid

CC sequences of novel human secreted proteins of the invention.
XX
SQ Sequence 143 AA;

Query Match 100.0%; Score 10; DB 22; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
|
Db 29 LVVYPWTQRF 38

RESULT 32
AAU30030
ID AAU30030 standard; Protein: 143 AA.

XX AAU30030;
XX
XX 18-DEC-2001 (first entry)

DE Novel human secreted protein #521.

KW Human: vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

OS Homo sapiens.

XX NO200179449-A2.

XX 25-OCT-2001.

PF 16-APR-2001; 2001WO-US08656.

PR 18-APR-2000; 2000US-0552929.

PR 26-JAN-2001; 2001US-0770160.

XX (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT;

DR WPI: 2001-611725/70.

XX Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy -
XX

PS Claim 20; Page 222-223; 765pp; English.

XX The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising
CC the nucleic acids encoding the polypeptides and cells genetically
CC engineered to express them are also useful for producing the proteins.
CC The proteins are useful in genetic vaccination, testing and
CC therapy, and can be used as nutritional supplements. They may be used to
CC increase stem cell proliferation; to regulate haematopoiesis; and in
CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
CC immune suppression and/or stimulation; as anti-inflammatory agents; and
CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid
CC sequences of novel human secreted proteins of the invention.

XX Sequence 143 AA;

Query Match 100.0%; Score 10; DB 22; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.00019;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
|
Db 29 LVVYPWTQRF 38

RESULT 33
AAU30083
ID AAU30083 standard; Protein: 143 AA.

XX AAU30083;

XX 18-DEC-2001 (first entry)

DE Novel human secreted protein #574.

KW Human: vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

OS Homo sapiens.

XX NO200179449-A2.

XX 25-OCT-2001.

PF 16-APR-2001; 2001WO-US08656.

PR 18-APR-2000; 2000US-0552929.

PR 26-JAN-2001; 2001US-0770160.

XX (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT;

DR WPI: 2001-611725/70.

XX Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy -
XX

PS Claim 20; Page 235; 765pp; English.

XX The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising
CC the nucleic acids encoding the polypeptides and cells genetically
CC engineered to express them are also useful for producing the proteins.
CC The proteins are useful in genetic vaccination, testing and
CC therapy, and can be used as nutritional supplements. They may be used to
CC increase stem cell proliferation; to regulate haematopoiesis; and in
CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
CC immune suppression and/or stimulation; as anti-inflammatory agents; and
CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid
CC sequences of novel human secreted proteins of the invention.

XX Sequence 143 AA;

Query Match 100.0%; Score 10; DB 22; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
|
Db 29 LVVYPWTQRF 38

XX WPI: 1993-167394/20.
 DR XX
 PT New haemoglobin variants bind reversibly to oxygen - useful as
 PT physiological oxygen carriers (e.g. in blood substitutes) and as
 PT plasma expanders
 XX
 PS Disclosure: Page 13; 211pp; English.
 XX
 CC The sequences given in AAR39721-28 represent variant haemoglobins
 CC derived from embryonic zeta, embryonic epsilon, fetal gamma, adult
 CC delta, adult alpha and adult beta haemoglobins. The variants HbF
 CC Chicago, Hb Portland Ritsville and Hb Bovill have lower oxygen affinity,
 CC HbA Deer Lodge, HbA Abruzzo and HbA McKees Rock have higher oxygen
 CC affinity. HbA Motom/Hacettepe is an alkaline stable variant compared
 CC to the wild-type molecules, and a further variant was produced which
 CC had a lower oxygen affinity and was stable in alkali. The DNA
 CC sequences encoding these globin variants may be used to transform
 CC yeasts such that they produce the globins. The variant globins may
 CC be used in applications which require physiological oxygen carriers,
 CC such as in blood substitute solutions, or as plasma expanders.
 CC
 SQ Sequence 144 AA:

Query Match 100.0%; Score 10; DB 14; Length 144;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVVYPWTORE 10
 |||||
 Db 32 LVVYPWTGRF 41

RESULT 39
 AAM73382
 ID AAM73382 standard; Protein; 144 AA.
 XX
 AC AAM73382;
 XX
 DT 18-FEB-1999 (first entry)
 XX
 DE Human haemoglobin beta-chain mutant Y145Stop.
 XX
 KW Haemoglobin; mutant; human; substitute blood product; synthetic blood;
 KW beta chain.
 XX
 OS Homo sapiens.
 XX
 PN US5827693-A.
 XX
 PD 27-OCT-1998.
 XX
 PF 07-JUN-1995; 95US-0484686.
 XX
 PR 29-APR-1992; 92US-0876290.
 PR 16-APR-1990; 90US-0509918.
 PR 14-NOV-1990; 90US-0614359.
 PR 12-APR-1991; 91US-0684611.
 PR 29-DEC-1994; 94US-0368407.
 PR 07-JUN-1995; 95US-0484686.
 XX
 PA (APEX-) APEX BIOSCIENCE INC.
 XX
 PI Bajwa W, Bonaventura J, De Angelo J, Motwani NN;
 XX
 DR WPI: 1998-593993/50.
 XX
 PT Recombinant expression of globin chains - and variants in yeast,
 PT useful as substitutes for natural blood required for oxygen carriage
 XX
 PS Claim 54; Page -, 144pp; English.
 XX

CC This sequence represents a human haemoglobin beta chain variant. DNA
 CC encoding this sequence is used in the recombinant DNA vector of the
 CC invention, which expresses a globin chain in a yeast cell, and comprises:
 CC (a) a first DNA sequence encoding a globin chain; (b) a yeast
 CC transcriptional promoter which promotes the transcription of the first
 CC DNA sequence; (c) a second DNA sequence encoding a yeast selectable
 CC marker; and (d) a yeast replication origin. The vectors and recombinant
 CC yeast cells containing them can be used for the recombinant production of
 CC the globin chains and their variants. The products in turn, can be used
 CC as substitute blood products, where oxygen carriage is required. The
 CC variants are designed to enable generally stable cross-linking of
 CC monomers to a tetrameric form, which does not dissociate into dimers.
 CC They are also designed to be stable to a certain extent in alkaline
 CC conditions compared to normal physiological conditions. The yeast strains
 CC used allow recombinant production of correctly processed haemoglobin
 CC chains in large quantities. The use of recombinant blood also eliminates
 CC risks of contamination of donated blood samples, and also shortages of
 CC N.B. This sequence was created from the human haemoglobin beta chain
 CC sequence given in the specification.
 CC
 SQ Sequence 144 AA:

Query Match 100.0%; Score 10; DB 19; Length 144;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVVYPWTORE 10
 |||||
 Db 32 LVVYPWTGRF 41

RESULT 40
 AAR20303
 ID AAR20303 standard; Protein; 145 AA.
 XX
 AC AAR20303;
 XX
 DT 13-APR-1992 (first entry)
 XX
 DE Val(1) to Met, His(2) deleted beta-globin mutant.
 XX
 KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb.
 XX
 OS Homo sapiens.
 XX
 PN WO9119505-A.
 XX
 PD 26-DEC-1991.
 XX
 PF 20-JUN-1991; 91WO-US04156.
 XX
 PR 20-JUN-1990; 90US-0541011.
 XX
 PA (RESF) RES CORP TECHN INC.
 XX
 PI Fronticelli C, Buccil E, Brinigar W;
 XX
 DR WPI: 1992-024191/03.
 XX
 PT Modified beta-chain of human haemoglobin - with aminoacid changes
 PT to reduce oxygen affinity, used in blood prods. for transfusion,
 PT with enhanced chloride sensitivity
 XX
 PS Claim 5; Page 60; 87pp; English.
 XX
 CC The modified beta-globin chain differs from the wild-type protein
 CC sequence in that it has Val at position 1 replaced by Met and His
 CC at position 2 deleted. It is one of the preferred mutant proteins
 CC covered by the invention having reduced oxygen affinity compared
 CC to wild-type beta-chain. See also AAO20236-8 and AAR20300-R20317.
 XX

SQ Sequence 145 AA;

Query Match 100.0%; Score 10; DB 13; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFGRF 10
| | | | | | | | | |
DB 31 LVVYPWTFGRF 40

RESULT 41

AAR20305 AAR20305 standard; Protein; 145 AA.

AC AAR20305;

XX 13-APR-1992 (first entry)

DE Val(1) to Met, His(2) deleted, Ala(76) to Lys beta-globin mutant.

XX autooxidation; beta-globin; blood transfusion; haemoglobin; Hb;

KM NAl (1) Val to Met; NA2 (2) His deleted; E20 (76) Ala to Lys.

XX Homo sapiens.

XX WO9119505-A.

XX 26-DEC-1991.

XX 20-JUN-1991; 91WO-US04156.

XX 20-JUN-1990; 90US-0541011.

XX (RESE) RES CORP TECHN INC.

XX Fronticelli C, Buccl E, Brinlgar W;

XX WPI; 1992-024191/03.

XX Modified beta-chain of human haemoglobin - with aminoacid changes

XX with enhanced chloride sensitivity

XX Claim 8: Page 60; 87pp; English.

XX The modified beta-globin chain differs from the wild-type protein

XX sequence in that it has Val at position 1 replaced by Met, His

XX at position 2 deleted and Ala at position 76 replaced by Lys. It is

XX one of the preferred mutant proteins covered by the invention having

XX reduced oxygen affinity compared to wild-type beta-chain.

XX See also AAQ20236-8 and AAR20300-R20317.

XX SQ Sequence 145 AA;

OY 1 LVVYPWTFGRF 10

DB 31 LVVYPWTFGRF 40

RESULT 42

AAR20306 AAR20306 standard; Protein; 145 AA.

XX AAR20306;

XX 13-APR-1992 (first entry)

XX Met(1), His(2) deleted, Lys(76), Arg(144) beta-globin mutant.

XX autooxidation; beta-globin; blood transfusion; haemoglobin; Hb;

KM NAl (1) Val to Met; NA2 (2) His deleted; E20 (76) Ala to Lys;

XX HCl (144) Lys to Arg.

XX Homo sapiens.

XX WO9119505-A.

XX 26-DEC-1991.

XX 20-JUN-1991; 91WO-US04156.

XX 20-JUN-1990; 90US-0541011.

XX (RESE) RES CORP TECHN INC.

XX Fronticelli C, Buccl E, Brinlgar W;

XX WPI; 1992-024191/03.

XX Claim 9: Page 61; 87pp; English.

XX The modified beta-globin chain differs from the wild-type protein

XX sequence in that it has Val at position 1 replaced by Met, His

XX at position 2 deleted, Ala at position 76 replaced by Lys and Lys

XX CC at position 144 replaced by Arg. It is one of the preferred mutant

XX proteins covered by the invention having reduced oxygen affinity

XX compared to wild-type beta-chain.

XX See also AAQ20236-8 and AAR20300-R20317.

XX SQ Sequence 145 AA;

OY 1 LVVYPWTFGRF 10

DB 31 LVVYPWTFGRF 40

RESULT 43

AAR20346 AAR20346 standard; Protein; 145 AA.

XX AAR20346;

XX 06-NOV-2001 (first entry)

XX Human polypeptide SEQ ID NO 24238.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;

XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;

XX tissue growth factor; immunomodulatory; cancer; leukaemia;

XX nervous system disorders; arthritis; inflammation.

XX Homo sapiens.

XX WO200164835-A2.

XX 07-SEP-2001.

XX 26-FEB-2001; 2001WO-US04927.

XX 28-FEB-2000; 2000US-0515126.

PR 18-MAY-2000; 2000US-0577409.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-514838/56.
DR N-PSDB; AAI90277.
XX
XX Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders.
XX
XX
PS Claim 20; SEQ ID NO 24238; 1399pp + Sequence Listing; English.
XX
XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
SQ Sequence 145 AA;

Query Match 100.0%; Score 10; DB 22; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTWQRF 10
Db 39 LVVYPTWQRF 48

RESULT 44

AAAP81301
ID AAP81301 standard; protein; 146 AA.

XX
AC AAP81301;

XX
DT 16-SEP-1990 (first entry)

XX
DE Mutant beta-globin sequence.

XX
KW Mutant beta-globin; artificial haemoglobin.

XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers

XX
FT Misc-difference 102..102 /label=Substituted amino acid

XX
FT Misc-difference 63..63 /note=Asn of known sequence replaced by Thr

XX
FT Misc-difference 67..67 /label=Substituted amino acid

XX
FT Misc-difference 67..67 /note=His of known sequence replaced by Phe

XX
FT Misc-difference 67..67 /label=Substituted amino acid

XX
PN W08809179-A.

XX
PD 01-DEC-1988.

XX
PF 13-MAY-1988; 88WO-US01534.
XX

PR 16-MAY-1987; 87GB-0011614.
XX
XX (SOMA-) SOMATOGENICS (MEDT-) MEDICAL RESEARCH COUNCIL.
XX
XX Hoffman SJ, Nagai K;
XX
XX WPI; 1988-353805/49.
DR N-PSDB; AAN80526.
XX
XX Recombinant mutant and artificial haemoglobin - used as blood substitutes
PT and for altering oxygen concns. in cell cultures or fluids.
XX
XX
PS Disclosure; 71pp; English.
XX
XX The sequence is a mutant of beta-globin. The mutant contains only
CC one of the three possible amino acid changes shown. It is expressed as a
CC fusion protein with the alpha globin sequence and a spacer peptide,
CC which is cleaved with Factor xa. Liberated alpha-globin is
CC combined with beta-globin from a non-blood source and a source of
CC haem to form synthetic haemoglobin. This is used in blood
CC substitute solutions, and mutant haemoglobins, whether of reduced or
CC enhanced oxygen affinity, may be of value for altering oxygen
CC concns. in cell cultures or extracting oxygen from fluids.
XX
XX
SQ Sequence 146 AA;

Query Match 100.0%; Score 10; DB 9; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTWQRF 10
Db 32 LVVYPTWQRF 41

RESULT 45

AAAR08115
ID AAR08115 standard; protein; 146 AA.

XX
AC AAR08115;

XX
DT 27-FEB-1991 (first entry)

XX
DE des-Val beta globin polypeptide.

XX
KW Polyclonon operon; di-alpha-globin; di-beta globin; haemoglobin;

XX
OS synthetic.

XX
PN W09013645-A.

XX
PD 15-NOV-1990.

XX
PF 10-MAY-1990; 90WO-US02654.

XX
PR 13-JUL-1989; 89US-0379116.

XX
PR 30-JUN-1989; 89US-0349623.

XX
PR 30-JUN-1989; 89US-0374161.

XX
PA (SOMA-) SOMATOGENICS INT.

XX
PI Hoffman SJ, Looker DL, Rosendal MS, Stetler GL, Wagenbach M;

XX
DR WPI; 1990-361480/48.

XX
DR N-PSDB; AAO06685.

XX
PT Di-alpha and di-beta globin-like polypeptide(s) - used for prodn.

XX
PT of haemoglobin having increased half-life and produced in
XX bacteria and yeast
XX
PS Disclosure; fig 12; 22pp; English.
XX

CC This beta globin polypeptide is encoded by one cistron of a polycistronic operon. It is expressed after the di-alpha polypeptide as the latter affects folding of the beta globin. This is essential for incorporation of the haem molecule to form functional haemoglobin. The synthetic haemoglobin produced on expression in CC a recombinant host, e.g. yeast, cell has an increased intravascular half life. See also AA006884.

XX
SQ Sequence 146 AA:

Query Match 100.0%; Score 10; DB 11; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFGRF 10
| | | | | | | | | |
DB 32 LVVYPWTFGRF 41

RESULT 46

AAR20302
ID AAR20302 standard; Protein; 146 AA.
XX
AC AAR20302;

DT 13-APR-1992 (first entry)

DE Mutant "E11 (67) Val to Thr" beta-globin.

KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb.

OS Homo sapiens.

PN W09119505-A.

PD 26-DEC-1991.

PF 20-JUN-1991; 91WO-US04156.

PR 20-JUN-1990; 90US-0541011.

PA (RESE) RES CORP TECHN INC.

PI Fronticell C, Buccl E, Brinigar W;

DR WPI; 1992-024191/03.

PT Modified beta-chain of human haemoglobin - with aminoacid changes to reduce oxygen affinity, used in blood prods. for transfusion, with enhanced chloride sensitivity

PS Claim 22; Page 10; 87pp; English.

CC In this modified beta-globin chain Val at position 67 has been replaced by Thr. It is one of the preferred mutant proteins covered by the invention having enhanced sensitivity toward chloride and a lower oxygen affinity than natural human Hb.

XX
SQ Sequence 146 AA:

Query Match 100.0%; Score 10; DB 13; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFGRF 10
| | | | | | | | | |
DB 32 LVVYPWTFGRF 41

RESULT 47
AAR20304

ID AAR20304 standard; Protein; 146 AA.

XX
AC AAR20304;

DT 13-APR-1992 (first entry)

DE "HCl Lys(144) to Arg" beta-globin mutant.

KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb.

OS Homo sapiens.

PN W09119505-A.

PD 26-DEC-1991.

PF 20-JUN-1991; 91WO-US04156.

PR 20-JUN-1990; 90US-0541011.

PA (RESE) RES CORP TECHN INC.

PI Fronticell C, Buccl E, Brinigar W;

DR WPI; 1992-024191/03.

PT Modified beta-chain of human haemoglobin - with aminoacid changes to reduce oxygen affinity, used in blood prods. for transfusion, with enhanced chloride sensitivity

PS Claim 6; Page 60; 87pp; English.

CC The modified beta-globin chain differs from the wild-type protein sequence in that it has Lys at position 144 replaced by Arg. It is one of the preferred mutant proteins covered by the invention having reduced oxygen affinity compared to wild-type beta-chain.

CC See also AA020236-8 and AAR20300-R20317.

XX
SQ Sequence 146 AA:

Query Match 100.0%; Score 10; DB 13; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFGRF 10
| | | | | | | | | |
DB 32 LVVYPWTFGRF 41

RESULT 48

AAR20307
ID AAR20307 standard; Protein; 146 AA.

AC AAR20307;

DT 13-APR-1992 (first entry)

DE Glu(3) beta-globin mutant.

KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb;

KW NA3 (3) Leu to Glu.

OS Homo sapiens.

PN W09119505-A.

PD 26-DEC-1991.

PF 20-JUN-1991; 91WO-US04156.

PR 20-JUN-1990; 90US-0541011.

PA (RESE) RES CORP TECHN INC.
 XX Fronticelli C, Buccl E, Brinigar W;
 XX WPI: 1992-024191/03.
 DR
 XX Modified beta-chain of human haemoglobin - with aminoacid changes
 PT to reduce oxygen affinity, used in blood prods. for transfusion,
 PT with enhanced chloride sensitivity
 XX
 PS Claim 10; Page 62; 87pp; English.
 XX
 CC The modified beta-globin chain differs from the wild-type protein
 CC sequence in that it has Leu at position 3 replaced by Glu. It is
 CC one of the preferred mutant proteins covered by the invention having
 CC reduced oxygen affinity compared to wild-type beta-chain.
 CC See also AAQ20236-8 and AAR20300-R20317.
 XX
 SQ Sequence 146 AA;

Query Match 100.0%; Score 10; DB 13; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
 |||||
 Db 32 LVVYPWTgrf 41

RESULT 49

AAR20308
 ID AAR20308 standard; Protein; 146 AA.
 XX
 AC AAR20308;
 XX
 DT 13-APR-1992 (first entry)
 XX
 DE Asp(3) beta-globin mutant.
 XX
 KM autoxidation; beta-globin; blood transfusion; haemoglobin; Hb;
 KW NA3 (3) Leu to Asp.
 XX
 OS Homo sapiens.
 XX
 PN WO9119505-A.
 XX
 PD 26-DEC-1991.
 XX
 PF 20-JUN-1991; 91WO-US04156.
 XX
 PR 20-JUN-1990; 90US-0541011.
 XX
 PA (RESE) RES CORP TECHN INC.
 XX
 PI Fronticelli C, Buccl E, Brinigar W;
 XX
 DR WPI: 1992-024191/03.
 XX
 PT Modified beta-chain of human haemoglobin - with aminoacid changes
 PT to reduce oxygen affinity, used in blood prods. for transfusion,
 PT with enhanced chloride sensitivity
 XX
 PS Claim 10; Page 62; 87pp; English.
 XX
 CC The modified beta-globin chain differs from the wild-type protein
 CC sequence in that it has Leu at position 3 replaced by Asp. It is
 CC one of the preferred mutant proteins covered by the invention having
 CC reduced oxygen affinity compared to wild-type beta-chain.
 CC See also AAQ20236-8 and AAR20300-R20317.
 XX
 SQ Sequence 146 AA;

Query Match 100.0%; Score 10; DB 13; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
 |||||
 Db 32 LVVYPWTgrf 41

RESULT 50

AAR20309
 ID AAR20309 standard; Protein; 146 AA.
 XX
 AC AAR20309;
 XX
 DT 13-APR-1992 (first entry)
 XX
 DE Glu(4) beta-globin mutant.
 XX
 KM autoxidation; beta-globin; blood transfusion; haemoglobin; Hb;
 KW A1 (4) Thr to Glu.
 XX
 OS Homo sapiens.
 XX
 PN WO9119505-A.
 XX
 PD 26-DEC-1991.
 XX
 PF 20-JUN-1991; 91WO-US04156.
 XX
 PR 20-JUN-1990; 90US-0541011.
 XX
 PA (RESE) RES CORP TECHN INC.
 XX
 PI Fronticelli C, Buccl E, Brinigar W;
 XX
 DR WPI: 1992-024191/03.
 XX
 PT Modified beta-chain of human haemoglobin - with aminoacid changes
 PT to reduce oxygen affinity, used in blood prods. for transfusion,
 PT with enhanced chloride sensitivity
 XX
 PS Claim 11; Page 62; 87pp; English.
 XX
 CC The modified beta-globin chain differs from the wild-type protein
 CC sequence in that it has Thr at position 4 replaced by Glu. It is
 CC one of the preferred mutant proteins covered by the invention having
 CC reduced oxygen affinity compared to wild-type beta-chain.
 CC See also AAQ20236-8 and AAR20300-R20317.
 XX
 SQ Sequence 146 AA;

Query Match 100.0%; Score 10; DB 13; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
 |||||
 Db 32 LVVYPWTgrf 41

RESULT 51

AAR20310
 ID AAR20310 standard; Protein; 146 AA.
 XX
 AC AAR20310;
 XX
 DT 13-APR-1992 (first entry)
 XX
 DE Asp(4) beta-globin mutant.
 XX

KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb;
KM A1 (4) Thr to Asp.
XX
XX Homo sapiens.
OS
XX
XX MO9119505-A.
XX
XX 26-DEC-1991.
PD
XX
XX 20-JUN-1991; 91WO-US04156.
PF
XX
XX 20-JUN-1990; 90US-0541011.
PR
XX
XX (RESE) RES CORP TECHN INC.
PA
XX
XX Fronticelli C, Buccl E, Brinigar W;
PI
XX
XX WPI; 1992-024191/03.
DR
XX
XX Modified beta-chain of human haemoglobin - with aminoacid changes
PT to reduce oxygen affinity, used in blood prods. for transfusion,
PT with enhanced chloride sensitivity
XX
XX
XX Claim 11; Page 62; 87pp; English.
PS
XX
XX The modified beta-globin chain differs from the wild-type protein
CC sequence in that it has Thr at position 4 replaced by Asp. It is
CC one of the preferred mutant proteins covered by the invention having
CC reduced oxygen affinity compared to wild-type beta-chain.
CC See also AAQ20236-8 and AAR20300-R20317.
CC
XX
XX Sequence 146 AA;
SQ

Query Match 100.0%; Score 10; DB 13; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTORF 10
|||
DB 32 LVVYPWTOGRF 41

RESULT 52
AAR20311
ID AAR20311 standard; Protein: 146 AA.
XX
XX AAR20311;
AC
XX
XX 13-APR-1992 (first entry)
DT
XX
XX Asp(5) beta-globin mutant.
DE
XX
XX autoxidation; beta-globin; blood transfusion; haemoglobin; Hb;
KM A2 (5) Pro to Asp.
KW
XX
XX Homo sapiens.
OS
XX
XX MO9119505-A.
PN
XX
XX 26-DEC-1991.
PD
XX
XX 20-JUN-1991; 91WO-US04156.
PF
XX
XX 20-JUN-1990; 90US-0541011.
PR
XX
XX (RESE) RES CORP TECHN INC.
PA
XX
XX Fronticelli C, Buccl E, Brinigar W;
PI
XX
XX WPI; 1992-024191/03.
DR
XX
XX Modified beta-chain of human haemoglobin - with aminoacid changes
PT

PT to reduce oxygen affinity, used in blood prods. for transfusion,
PT with enhanced chloride sensitivity
XX
XX
XX Claim 12; Page 62; 87pp; English.
PS
XX
XX The modified beta-globin chain differs from the wild-type protein
CC sequence in that it has Pro at position 5 replaced by Asp. It is
CC one of the preferred mutant proteins covered by the invention having
CC reduced oxygen affinity compared to wild-type beta-chain.
CC See also AAQ20236-8 and AAR20300-R20317.
CC
XX
XX Sequence 146 AA;
SQ

Query Match 100.0%; Score 10; DB 13; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTORF 10
|||
DB 32 LVVYPWTOGRF 41

RESULT 53
AAR20312
ID AAR20312 standard; Protein: 146 AA.
XX
XX AAR20312;
AC
XX
XX 13-APR-1992 (first entry)
DT
XX
XX Glu(5) beta-globin mutant.
DE
XX
XX autoxidation; beta-globin; blood transfusion; haemoglobin; Hb;
KM A2 (5) Pro to Glu.
KW
XX
XX Homo sapiens.
OS
XX
XX MO9119505-A.
PN
XX
XX 26-DEC-1991.
PD
XX
XX 20-JUN-1991; 91WO-US04156.
PF
XX
XX 20-JUN-1990; 90US-0541011.
PR
XX
XX (RESE) RES CORP TECHN INC.
PA
XX
XX Fronticelli C, Buccl E, Brinigar W;
PI
XX
XX WPI; 1992-024191/03.
DR
XX
XX Modified beta-chain of human haemoglobin - with aminoacid changes
PT to reduce oxygen affinity, used in blood prods. for transfusion,
PT with enhanced chloride sensitivity
XX
XX
XX Claim 12; Page 62; 87pp; English.
PS
XX
XX The modified beta-globin chain differs from the wild-type protein
CC sequence in that it has Pro at position 5 replaced by Glu. It is
CC one of the preferred mutant proteins covered by the invention having
CC reduced oxygen affinity compared to wild-type beta-chain.
CC See also AAQ20236-8 and AAR20300-R20317.
CC
XX
XX Sequence 146 AA;
SQ

Query Match 100.0%; Score 10; DB 13; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTORF 10
|||
DB 32 LVVYPWTOGRF 41

Db 32 lvvyptgrf 41

RESULT 54
ID AAR20313 standard; Protein; 146 AA.
XX
AC AAR20313;
XX
DT 13-APR-1992 (first entry)
XX
DE Gly(5) beta-globin mutant.
XX
KM autoxidation; beta-globin; blood transfusion; haemoglobin; Hb;
XX A2 (5) Pro to Gly.
XX
OS Homo sapiens.
XX
PN WO9119505-A.
XX
PD 26-DEC-1991.
XX
PF 20-JUN-1991; 91WO-US04156.
XX
PR 20-JUN-1990; 90US-0541011.
XX
PS (RESE) RES CORP TECHN INC.
XX
PI Fronticelli C, Buccì E, Brinigar W;
XX
DR WPI; 1992-024191/03.
XX
PT Modified beta-chain of human haemoglobin - with aminoacid changes
PT to reduce oxygen affinity, used in blood prods. for transfusion,
PT with enhanced chloride sensitivity
XX
PS Claim 13; Page 62; 87pp; English.
XX
CC The modified beta-globin chain differs from the wild-type protein
CC sequence in that it has Pro at position 5 replaced by Gly. It is
CC one of the preferred mutant proteins covered by the invention having
CC reduced oxygen affinity compared to wild-type beta-chain.
CC See also AAO20236-8 and AAR20300-R20317.
XX
SQ Sequence 146 AA;

Query Match 100.0%; Score 10; DB 13; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
|||
Db 32 lvvyptgrf 41

RESULT 55
ID AAR20314 standard; Protein; 146 AA.
XX
AC AAR20314;
XX
DT 13-APR-1992 (first entry)
XX
DE Ala(5) beta-globin mutant.
XX
KM autoxidation; beta-globin; blood transfusion; haemoglobin; Hb;
XX A2 (5) Pro to Ala.
XX
OS Homo sapiens.
XX
PN WO9119505-A.
XX

PD 26-DEC-1991.
XX
PF 20-JUN-1991; 91WO-US04156.
XX
PR 20-JUN-1990; 90US-0541011.
XX
PA (RESE) RES CORP TECHN INC.
XX
PI Fronticelli C, Buccì E, Brinigar W;
XX
DR WPI; 1992-024191/03.
XX
PT Modified beta-chain of human haemoglobin - with aminoacid changes
PT to reduce oxygen affinity, used in blood prods. for transfusion,
PT with enhanced chloride sensitivity
XX
PS Claim 13; Page 62; 87pp; English.
XX
CC The modified beta-globin chain differs from the wild-type protein
CC sequence in that it has Pro at position 5 replaced by Ala. It is
CC one of the preferred mutant proteins covered by the invention having
CC reduced oxygen affinity compared to wild-type beta-chain.
CC See also AAO20236-8 and AAR20300-R20317.
XX
SQ Sequence 146 AA;

Query Match 100.0%; Score 10; DB 13; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
|||
Db 32 lvvyptgrf 41

RESULT 56
ID AAR20315 standard; Protein; 146 AA.
XX
AC AAR20315;
XX
DT 13-APR-1992 (first entry)
XX
DE Glu(69) beta-globin mutant.
XX
KM autoxidation; beta-globin; blood transfusion; haemoglobin; Hb;
XX E13 (69) Gly to Glu.
XX
OS Homo sapiens.
XX
PN WO9119505-A.
XX
PD 26-DEC-1991.
XX
PF 20-JUN-1991; 91WO-US04156.
XX
PR 20-JUN-1990; 90US-0541011.
XX
PS (RESE) RES CORP TECHN INC.
XX
PI Fronticelli C, Buccì E, Brinigar W;
XX
DR WPI; 1992-024191/03.
XX
PT Modified beta-chain of human haemoglobin - with aminoacid changes
PT to reduce oxygen affinity, used in blood prods. for transfusion,
PT with enhanced chloride sensitivity
XX
PS Claim 14; Page 62; 87pp; English.
XX
CC The modified beta-globin chain differs from the wild-type protein
CC sequence in that it has Gly at position 69 replaced by Glu. It is

CC one of the preferred mutant proteins covered by the invention having
 CC reduced oxygen affinity compared to wild-type beta-chain.
 CC See also AAQ20236-8 and AAR20300-R20317.
 XX
 SO Sequence 146 AA:

Query Match 100.0%; Score 10; DB 13; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
 |||||
 DB 32 LVVYPWTQRF 41

RESULT 57

AAR20316
 ID AAR20316 standard; Protein: 146 AA.

AC AAR20316;

DT 13-APR-1992 (first entry)

DE Asp(69) beta-globin mutant.

KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb;

KM E13 (69) Gly to Asp.

XX Homo sapiens.

PN WO9119505-A.

PD 26-DEC-1991.

PE 20-JUN-1991; 91WO-US04156.

PR 20-JUN-1990; 90US-0541011.

PA (RESE) RES CORP TECHN INC.

PI Fronticelli C, Buccl E, Brinlgar W;

DR WPI; 1992-024191/03.

PT Modified beta-chain of human haemoglobin - with aminoacid changes
 PT to reduce oxygen affinity, used in blood prods. for transfusion,
 PT with enhanced chloride sensitivity

PS Claim 14; Page 62; 87pp; English.

CC The modified beta-globin chain differs from the wild-type protein
 CC sequence in that it has Gly at position 69 replaced by Asp. It is
 CC one of the preferred mutant proteins covered by the invention having
 CC reduced oxygen affinity compared to wild-type beta-chain.
 CC See also AAQ20236-8 and AAR20300-R20317.

XX
 SO Sequence 146 AA:

Query Match 100.0%; Score 10; DB 13; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
 |||||
 DB 32 LVVYPWTQRF 41

RESULT 58

AAR20317
 ID AAR20317 standard; Protein: 146 AA.

AC AAR20317;

DT 13-APR-1992 (first entry)

DE Thr(70) beta-globin mutant.

KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb;

KM E14 (70) Ala to Thr.

XX Homo sapiens.

PN WO9119505-A.

PD 26-DEC-1991.

PE 20-JUN-1991; 91WO-US04156.

PR 20-JUN-1990; 90US-0541011.

PA (RESE) RES CORP TECHN INC.

PI Fronticelli C, Buccl E, Brinlgar W;

DR WPI; 1992-024191/03.

PT Modified beta-chain of human haemoglobin - with aminoacid changes
 PT to reduce oxygen affinity, used in blood prods. for transfusion,
 PT with enhanced chloride sensitivity

PS Claim 15; Page 63; 87pp; English.

CC The modified beta-globin chain differs from the wild-type protein
 CC sequence in that it has Ala at position 70 replaced by Thr. It is
 CC one of the preferred mutant proteins covered by the invention having
 CC reduced oxygen affinity compared to wild-type beta-chain.
 CC See also AAQ20236-8 and AAR20300-R20317.

XX
 SO Sequence 146 AA:

Query Match 100.0%; Score 10; DB 13; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
 |||||
 DB 32 LVVYPWTQRF 41

RESULT 59

AAR21914
 ID AAR21914 standard; Protein: 146 AA.

AC AAR21914;

DT 13-APR-1992 (first entry)

DE Ser(70) beta-globin mutant.

KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb;

KM E14 (70) Ala to Ser.

XX Homo sapiens.

PN WO9119505-A.

PD 26-DEC-1991.

PE 20-JUN-1991; 91WO-US04156.

PR 20-JUN-1990; 90US-0541011.

PA (RESE) RES CORP TECHN INC.

XX Fronticelli C, Buccl E, Brinigar W;
 XX WPI; 1992-024191/03.
 XX Modified beta-chain of human haemoglobin - with aminoacid changes
 PT to reduce oxygen affinity, used in blood prods. for transfusion,
 PT with enhanced chloride sensitivity
 XX
 PS Claim 15; Page 63; 87pp; English.
 XX
 CC The modified beta-globin chain differs from the wild-type protein
 CC sequence in that it has Ala at position 70 replaced by Ser. It is
 CC one of the preferred mutant proteins covered by the invention having
 CC reduced oxygen affinity compared to wild-type beta-chain.
 CC See also AAQ20236-8 and AAR20300-R20317.
 XX
 SQ Sequence 146 AA;

Query Match 100.0%; Score 10; DB 13; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 LVVYPWTQRF 10
 |||||
 DB 32 LVVYPWTQRF 41

RESULT 60
 AAR21915
 ID AAR21915 standard; Protein; 146 AA.
 AC AAR21915;
 XX
 DF 13-APR-1992 (first entry)
 XX
 DE Cys(75) beta-globin mutant.
 XX
 KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb;
 KM E19 (75) Leu to Cys.
 XX
 OS Homo sapiens.
 XX
 PN WO9119505-A.
 XX
 PD 26-DEC-1991.
 XX
 PF 20-JUN-1991; 91WO-US04156.
 XX
 PR 20-JUN-1990; 90US-0541011.
 XX
 PA (RESE) RES CORP TECHN INC.
 XX
 PI Fronticelli C, Buccl E, Brinigar W;
 XX
 DR WPI; 1992-024191/03.
 XX
 PT Modified beta-chain of human haemoglobin - with aminoacid changes
 PT to reduce oxygen affinity, used in blood prods. for transfusion,
 PT with enhanced chloride sensitivity
 XX
 PS Claim 16; Page 63; 87pp; English.
 XX
 CC The modified beta-globin chain differs from the wild-type protein
 CC sequence in that it has Leu at position 75 replaced by Cys. It is
 CC one of the preferred mutant proteins covered by the invention having
 CC reduced oxygen affinity compared to wild-type beta-chain.
 CC See also AAQ20236-8, AAR20300-R20317 and AAR21914-R21930.
 XX
 SQ Sequence 146 AA;

Query Match 100.0%; Score 10; DB 13; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 LVVYPWTQRF 10
 |||||
 DB 32 LVVYPWTQRF 41

RESULT 61
 AAR21916
 ID AAR21916 standard; Protein; 146 AA.
 AC AAR21916;
 XX
 DF 13-APR-1992 (first entry)
 XX
 DE Met(75) beta-globin mutant.
 XX
 KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb;
 KM E19 (75) Leu to Met.
 XX
 OS Homo sapiens.
 XX
 PN WO9119505-A.
 XX
 PD 26-DEC-1991.
 XX
 PF 20-JUN-1991; 91WO-US04156.
 XX
 PR 20-JUN-1990; 90US-0541011.
 XX
 PA (RESE) RES CORP TECHN INC.
 XX
 PI Fronticelli C, Buccl E, Brinigar W;
 XX
 DR WPI; 1992-024191/03.
 XX
 PT Modified beta-chain of human haemoglobin - with aminoacid changes
 PT to reduce oxygen affinity, used in blood prods. for transfusion,
 PT with enhanced chloride sensitivity
 XX
 PS Claim 16; Page 63; 87pp; English.
 XX
 CC The modified beta-globin chain differs from the wild-type protein
 CC sequence in that it has Leu at position 75 replaced by Met. It is
 CC one of the preferred mutant proteins covered by the invention having
 CC reduced oxygen affinity compared to wild-type beta-chain.
 CC See also AAQ20236-8, AAR20300-R20317 and AAR21914-R21930.
 XX
 SQ Sequence 146 AA;

Query Match 100.0%; Score 10; DB 13; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 LVVYPWTQRF 10
 |||||
 DB 32 LVVYPWTQRF 41

RESULT 62
 AAR21917
 ID AAR21917 standard; Protein; 146 AA.
 AC AAR21917;
 XX
 DF 13-APR-1992 (first entry)
 XX
 DE Arg(76) beta-globin mutant.
 XX
 KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb;

KW E20 (76) Ala to Arg.
 XX Homo sapiens.
 OS WO9119505-A.
 PN 26-DEC-1991.
 XX 20-JUN-1991; 91WO-US04156.
 PF 20-JUN-1990; 90US-0541011.
 PR (RESE) RES CORP TECHN INC.
 PA Fronticell1 C, Bucc1 E, Brinigar W;
 XX WPI: 1992-024191/03.
 DR Modified beta-chain of human haemoglobin - with aminoacid changes
 XX to reduce oxygen affinity, used in blood prods. for transfusion,
 PT with enhanced chloride sensitivity
 PS Claim 17; Page 63; 87pp; English.
 CC The modified beta-globin chain differs from the wild-type protein
 CC sequence in that it has Ala at position 76 replaced by Arg. It is
 CC one of the preferred mutant proteins covered by the invention having
 CC reduced oxygen affinity compared to wild-type beta-chain.
 CC See also AAQ20236-8, AAR20300-R20317 and AAR21914-R21930.
 XX
 SQ Sequence 146 AA:

Query Match 100.0%; Score 10; DB 13; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 LVVYPWTFORF 10
 |||||
 DB 32 LVVYPWTFGRF 41

RESULT 63
 AAR21918
 ID AAR21918 standard; Protein; 146 AA.
 AC AAR21918;
 XX 13-APR-1992 (first entry)
 DT His(76) beta-globin mutant.
 XX autooxidation; beta-globin; blood transfusion; haemoglobin; Hb;
 KW E20 (76) Ala to His.
 XX Homo sapiens.
 OS WO9119505-A.
 PN 26-DEC-1991.
 XX 20-JUN-1991; 91WO-US04156.
 PF 20-JUN-1990; 90US-0541011.
 PR (RESE) RES CORP TECHN INC.
 PA Fronticell1 C, Bucc1 E, Brinigar W;
 XX WPI: 1992-024191/03.
 DR Modified beta-chain of human haemoglobin - with aminoacid changes
 PT to reduce oxygen affinity, used in blood prods. for transfusion,

PT with enhanced chloride sensitivity
 XX Claim 17; Page 63; 87pp; English.
 PS The modified beta-globin chain differs from the wild-type protein
 CC sequence in that it has Ala at position 76 replaced by His. It is
 CC one of the preferred mutant proteins covered by the invention having
 CC reduced oxygen affinity compared to wild-type beta-chain.
 CC See also AAQ20236-8, AAR20300-R20317 and AAR21914-R21930.
 XX
 SQ Sequence 146 AA:

Query Match 100.0%; Score 10; DB 13; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 LVVYPWTFORF 10
 |||||
 DB 32 LVVYPWTFGRF 41

RESULT 64
 AAR21919
 ID AAR21919 standard; Protein; 146 AA.
 AC AAR21919;
 XX 13-APR-1992 (first entry)
 DT Lys(76) beta-globin mutant.
 XX autooxidation; beta-globin; blood transfusion; haemoglobin; Hb;
 KW E20 (76) Ala to Lys.
 XX Homo sapiens.
 OS WO9119505-A.
 PN 26-DEC-1991.
 XX 20-JUN-1991; 91WO-US04156.
 PF 20-JUN-1990; 90US-0541011.
 PR (RESE) RES CORP TECHN INC.
 PA Fronticell1 C, Bucc1 E, Brinigar W;
 XX WPI: 1992-024191/03.
 DR Modified beta-chain of human haemoglobin - with aminoacid changes
 PT to reduce oxygen affinity, used in blood prods. for transfusion,
 PT with enhanced chloride sensitivity
 PS Claim 17; Page 63; 87pp; English.
 CC The modified beta-globin chain differs from the wild-type protein
 CC sequence in that it has Ala at position 76 replaced by Lys. It is
 CC one of the preferred mutant proteins covered by the invention having
 CC reduced oxygen affinity compared to wild-type beta-chain.
 CC See also AAQ20236-8, AAR20300-R20317 and AAR21914-R21930.
 XX
 SQ Sequence 146 AA:

Query Match 100.0%; Score 10; DB 13; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 LVVYPWTFORF 10
 |||||
 DB 32 LVVYPWTFGRF 41

RESULT 65

AAR21920 standard; Protein; 146 AA.

AAR21920;

13-APR-1992 (first entry)

Met(1) beta-globin mutant.

autoxidation; beta-globin; blood transfusion; haemoglobin; HB;

NAI (1) Val to Met.

Homo sapiens.

WO9119505-A.

26-DEC-1991.

20-JUN-1991; 91WO-US04156.

20-JUN-1990; 90US-0541011.

(RESE) RES CORP TECHN INC.

Fronticell C, Buccl E, Brinlgar W;

WPI; 1992-024191/03.

Modified beta-chain of human haemoglobin - with aminoacid changes

to reduce oxygen affinity, used in blood prods. for transfusion,

with enhanced chloride sensitivity

Claim 18; Page 63; 87pp; English.

The modified beta-globin chain differs from the wild-type protein

sequence in that it has Val at position 1 replaced by Met. It is

one of the preferred mutant proteins covered by the invention having

reduced oxygen affinity compared to wild-type beta-chain.

See also AAQ20236-8, AAR20300-R20317 and AAR21914-R21930.

Query Match 100.0%; Score 10; DB 13; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00019;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LVVYPWTQRF 10

32 LVVYPWTQRF 41

13-APR-1992 (first entry)

Leu(1) human beta-globin mutant.

autoxidation; beta-globin; blood transfusion; haemoglobin; HB;

NAI (1) Val to Leu.

Homo sapiens.

WO9119505-A.

26-DEC-1991.

20-JUN-1991; 91WO-US04156.

20-JUN-1990; 90US-0541011.

(RESE) RES CORP TECHN INC.

Fronticell C, Buccl E, Brinlgar W;

WPI; 1992-024191/03.

Modified beta-chain of human haemoglobin - with aminoacid changes

to reduce oxygen affinity, used in blood prods. for transfusion,

with enhanced chloride sensitivity

Claim 18; Page 63; 87pp; English.

The modified beta-globin chain differs from the wild-type protein

sequence in that it has Val at position 1 replaced by Leu. It is

one of the preferred mutant proteins covered by the invention having

reduced oxygen affinity compared to wild-type beta-chain.

See also AAQ20236-8, AAR20300-R20317 and AAR21914-R21930.

Query Match 100.0%; Score 10; DB 13; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00019;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LVVYPWTQRF 10

32 LVVYPWTQRF 41

13-APR-1992 (first entry)

Leu(2) human beta-globin mutant.

autoxidation; beta-globin; blood transfusion; haemoglobin; HB;

NA2 (2) His to Leu.

Homo sapiens.

WO9119505-A.

26-DEC-1991.

20-JUN-1991; 91WO-US04156.

20-JUN-1990; 90US-0541011.

(RESE) RES CORP TECHN INC.

Fronticell C, Buccl E, Brinlgar W;

WPI; 1992-024191/03.

Modified beta-chain of human haemoglobin - with aminoacid changes

to reduce oxygen affinity, used in blood prods. for transfusion,

with enhanced chloride sensitivity

Claim 19; Page 63; 87pp; English.

The modified beta-globin chain differs from the wild-type protein

sequence in that it has His at position 2 replaced by Leu. It is

one of the preferred mutant proteins covered by the invention having

CC reduced oxygen affinity compared to wild-type beta-chain.
 CC See also AAQ20236-B, AAR20300-R20317 and AAR21914-R21930.
 XX
 SO Sequence 146 AA;

Query Match 100.0%; Score 10; DB 13; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 LVVYPWTORF 10
 DB 32 LVVYPWTORF 41

RESULT 68
 AAR21923
 ID AAR21923 standard; Protein: 146 AA.
 XX
 AC AAR21923;

XX 13-APR-1992 (first entry)
 DE Tyr(2) human beta-globin mutant.
 XX
 KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb;
 KM NA2 (2) His to Tyr.
 XX

OS Homo sapiens.
 XX
 PN MO9119505-A.
 PD 26-DEC-1991.
 XX
 PF 20-JUN-1991; 91WO-US04156.
 XX
 PR 20-JUN-1990; 90US-0541011.
 XX
 PA (RESE) RES CORP TECHN INC.
 XX
 PI Fronticelli C, Buccell E, Brinigar W;
 XX
 DR WPI: 1992-024191/03.

XX Modified beta-chain of human haemoglobin - with aminoacid changes
 PT to reduce oxygen affinity, used in blood prods. for transfusion,
 PT with enhanced chloride sensitivity

PS Claim 19; Page 63; 87pp: English.

XX The modified beta-globin chain differs from the wild-type protein
 CC sequence in that it has His at position 2 replaced by Tyr. It is
 CC one of the preferred mutant proteins covered by the invention having
 CC reduced oxygen affinity compared to wild-type beta-chain.
 CC See also AAQ20236-B, AAR20300-R20317 and AAR21914-R21930.
 XX

SO Sequence 146 AA;

Query Match 100.0%; Score 10; DB 13; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORF 10
 DB 32 LVVYPWTORF 41

RESULT 69
 AAR21924
 ID AAR21924 standard; Protein: 146 AA.
 XX
 AC AAR21924;

XX 13-APR-1992 (first entry)
 DE Asp(2) human beta-globin mutant.
 XX

KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb;
 KM NA2 (2) His to Asp.
 XX

OS Homo sapiens.
 XX
 PN MO9119505-A.
 PD 26-DEC-1991.
 XX
 PF 20-JUN-1991; 91WO-US04156.
 XX
 PR 20-JUN-1990; 90US-0541011.
 XX
 PA (RESE) RES CORP TECHN INC.
 XX
 PI Fronticelli C, Buccell E, Brinigar W;
 XX
 DR WPI: 1992-024191/03.

XX Modified beta-chain of human haemoglobin - with aminoacid changes
 PT to reduce oxygen affinity, used in blood prods. for transfusion,
 PT with enhanced chloride sensitivity

PS Claim 19; Page 63; 87pp: English.

XX The modified beta-globin chain differs from the wild-type protein
 CC sequence in that it has His at position 2 replaced by Asp. It is
 CC one of the preferred mutant proteins covered by the invention having
 CC reduced oxygen affinity compared to wild-type beta-chain.
 CC See also AAQ20236-B, AAR20300-R20317 and AAR21914-R21930.
 XX

SO Sequence 146 AA;

Query Match 100.0%; Score 10; DB 13; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORF 10
 DB 32 LVVYPWTORF 41

RESULT 70
 AAR21925
 ID AAR21925 standard; Protein: 146 AA.
 XX
 AC AAR21925;

XX 13-APR-1992 (first entry)
 DE Met(1), Leu(2) human beta-globin mutant.
 XX

KW autoxidation; beta-globin; blood transfusion; haemoglobin; Hb.
 KM
 XX

OS Homo sapiens.
 XX
 PN MO9119505-A.
 PD 26-DEC-1991.
 XX
 PF 20-JUN-1991; 91WO-US04156.
 XX
 PR 20-JUN-1990; 90US-0541011.
 XX
 PA (RESE) RES CORP TECHN INC.
 XX
 PI Fronticelli C, Buccell E, Brinigar W;

XX MPI; 1992-024191/03.

XX Modified beta-chain of human haemoglobin - with aminoacid changes
PT to reduce oxygen affinity, used in blood prods. for transfusion,
XX with enhanced chloride sensitivity

PS Claim 20; Page 63; 87pp; English.

XX The modified beta-globin chain differs from the wild-type protein
CC sequence in that it has Val at position 1 replaced by Met and His at
CC position 2 replaced by Leu. It is one of the preferred mutant proteins
CC covered by the invention having reduced oxygen affinity compared to
CC wild-type beta-chain.
CC See also AAQ20236-8, AAR20300-R20317 and AAR21914-R21930.

XX Sequence 146 AA;

Query Match

Best Local Similarity 100.0%; Score 10; DB 13; Length 146;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
|||
Db 32 LVVYPWTQRF 41

RESULT 71

AAR21926
ID AAR21926 standard; Protein; 146 AA.

AC AAR21926;

DT 13-APR-1992 (first entry)

DE Met(1), Asp(2) human beta-globin mutant.

XX autooxidation; beta-globin; blood transfusion; haemoglobin; Hb.

OS Homo sapiens.

XX MO9119505-A.

XX 26-DEC-1991.

XX 20-JUN-1991; 91WO-US04156.

XX 20-JUN-1990; 90US-0541011.

XX (RESE) RES CORP TECHN INC.

PI Fronticelli C, Buccì E, Brinigar W;

DR MPI; 1992-024191/03.

XX Modified beta-chain of human haemoglobin - with aminoacid changes
PT to reduce oxygen affinity, used in blood prods. for transfusion,
XX with enhanced chloride sensitivity

PS Claim 20; Page 63; 87pp; English.

XX The modified beta-globin chain differs from the wild-type protein
CC sequence in that it has Val at position 1 replaced by Met and His at
CC position 2 replaced by Asp. It is one of the preferred mutant proteins
CC covered by the invention having reduced oxygen affinity compared to
CC wild-type beta-chain.
CC See also AAQ20236-8, AAR20300-R20317 and AAR21914-R21930.

XX Sequence 146 AA;

Query Match

Best Local Similarity 100.0%; Score 10; DB 13; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
|||
Db 32 LVVYPWTQRF 41

RESULT 72

AAR21927
ID AAR21927 standard; Protein; 146 AA.

AC AAR21927;

DT 13-APR-1992 (first entry)

DE Met(1), Tyr(2) human beta-globin mutant.

XX autooxidation; beta-globin; blood transfusion; haemoglobin; Hb.

OS Homo sapiens.

XX MO9119505-A.

XX 26-DEC-1991.

XX 20-JUN-1991; 91WO-US04156.

XX 20-JUN-1990; 90US-0541011.

XX (RESE) RES CORP TECHN INC.

PI Fronticelli C, Buccì E, Brinigar W;

DR MPI; 1992-024191/03.

XX Modified beta-chain of human haemoglobin - with aminoacid changes
PT to reduce oxygen affinity, used in blood prods. for transfusion,
XX with enhanced chloride sensitivity

PS Claim 20; Page 63; 87pp; English.

XX The modified beta-globin chain differs from the wild-type protein
CC sequence in that it has Val at position 1 replaced by Met and His at
CC position 2 replaced by Tyr. It is one of the preferred mutant proteins
CC covered by the invention having reduced oxygen affinity compared to
CC wild-type beta-chain.
CC See also AAQ20236-8, AAR20300-R20317 and AAR21914-R21930.

XX Sequence 146 AA;

Query Match

Best Local Similarity 100.0%; Score 10; DB 13; Length 146;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
|||
Db 32 LVVYPWTQRF 41

RESULT 73

AAR21928
ID AAR21928 standard; Protein; 146 AA.

AC AAR21928;

DT 13-APR-1992 (first entry)

DE Leu(1), Leu(2) human beta-globin mutant.

XX autooxidation; beta-globin; blood transfusion; haemoglobin; Hb.

OS Homo sapiens.
XX
XX WO9119505-A.
XX
XX 26-DEC-1991.
XX
XX
XX 20-JUN-1991; 91WO-US04156.
XX
XX 20-JUN-1990; 90US-0541011.
XX
XX (RESE) RES CORP TECHN INC.
XX
XX Fronticell C, Buccl E, Brinlgar W;
XX WPI; 1992-024191/03.
XX
XX Modified beta-chain of human haemoglobin - with aminoacid changes
PT to reduce oxygen affinity, used in blood prods. for transfusion,
PT with enhanced chloride sensitivity
XX
XX
XX Claim 20; Page 63; 87pp; English.
XX
XX
CC The modified beta-globin chain differs from the wild-type protein
CC sequence in that it has Val at position 1 replaced by Leu and His at
CC position 2 replaced by Leu. It is one of the preferred mutant proteins
CC covered by the invention having reduced oxygen affinity compared to
CC wild-type beta-chain.
CC See also AAO20236-8, AAR20300-R20317 and AAR21914-R21930.
CC
XX
SQ Sequence 146 AA:

Query Match 100.0%; Score 10; DB 13; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
DB 32 LVVYPWTQRF 41

RESULT 74
AAR21929
ID AAR21929 standard; Protein; 146 AA.
XX
XX AAR21929;
XX
XX 13-APR-1992 (first entry)
XX
XX Leu(1), Asp(2) human beta-globin mutant.
XX
XX autoxidation; beta-globin; blood transfusion; haemoglobin; HB.
XX
XX Homo sapiens.
XX
XX WO9119505-A.
XX
XX 26-DEC-1991.
XX
XX 20-JUN-1991; 91WO-US04156.
XX
XX 20-JUN-1990; 90US-0541011.
XX
XX (RESE) RES CORP TECHN INC.
XX
XX Fronticell C, Buccl E, Brinlgar W;
XX WPI; 1992-024191/03.
XX
XX Modified beta-chain of human haemoglobin - with aminoacid changes
PT to reduce oxygen affinity, used in blood prods. for transfusion,
PT with enhanced chloride sensitivity
XX

PS Claim 20; Page 63; 87pp; English.
XX
XX The modified beta-globin chain differs from the wild-type protein
CC sequence in that it has Val at position 1 replaced by Leu and His at
CC position 2 replaced by Asp. It is one of the preferred mutant proteins
CC covered by the invention having reduced oxygen affinity compared to
CC wild-type beta-chain.
CC See also AAO20236-8, AAR20300-R20317 and AAR21914-R21930.
CC
XX
SQ Sequence 146 AA:

Query Match 100.0%; Score 10; DB 13; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
DB 32 LVVYPWTQRF 41

RESULT 75
AAR21930
ID AAR21930 standard; Protein; 146 AA.
XX
XX AAR21930;
XX
XX 13-APR-1992 (first entry)
XX
XX Leu(1), Tyr(2) human beta-globin mutant.
XX
XX autoxidation; beta-globin; blood transfusion; haemoglobin; HB.
XX
XX Homo sapiens.
XX
XX WO9119505-A.
XX
XX 26-DEC-1991.
XX
XX 20-JUN-1991; 91WO-US04156.
XX
XX 20-JUN-1990; 90US-0541011.
XX
XX (RESE) RES CORP TECHN INC.
XX
XX Fronticell C, Buccl E, Brinlgar W;
XX WPI; 1992-024191/03.
XX
XX Modified beta-chain of human haemoglobin - with aminoacid changes
PT to reduce oxygen affinity, used in blood prods. for transfusion,
PT with enhanced chloride sensitivity
XX
XX Claim 20; Page 63; 87pp; English.
XX
XX The modified beta-globin chain differs from the wild-type protein
CC sequence in that it has Val at position 1 replaced by Leu and His at
CC position 2 replaced by Tyr. It is one of the preferred mutant proteins
CC covered by the invention having reduced oxygen affinity compared to
CC wild-type beta-chain.
CC See also AAO20236-8, AAR20300-R20317 and AAR21914-R21929.
CC
XX
SQ Sequence 146 AA:

Query Match 100.0%; Score 10; DB 13; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
DB 32 LVVYPWTQRF 41

```

RESULT 76
ID AAR29609 standard; Protein; 146 AA.
XX
XX AAR29609;
AC
XX
DT 15-JAN-1993 (first entry)
XX
XX Mutant human beta-globin 2.
DE
XX Polymerisation intramolecular crosslink; oxygen exchange; erythrocytes;
KM HIV.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH misc_difference 9 /*tag= a
FT /label= beta_9_Ser_to_Cys
FT
XX
XX W09211283-A.
PN
XX
XX 09-JUL-1992.
PD
XX
XX 20-DEC-1991; 91WO-US09624.
PF
XX
XX 20-DEC-1990; 90US-0630825.
PR
XX
XX (UYAL-) UNIV ALABAMA RES FOUND.
PA
XX
XX McCune SL, Townes TM.
PI
XX
XX WPI; 1992-250026/30.
DR
XX N-PSDB; AAQ26427.
DR
XX
XX Transgenic, crosslinked polymeric human haemoglobin - useful as a
PT cell-free blood substitute
PT
XX
XX Disclosure; Page 13; 42pp; English.
XX
XX This sequence was not disclosed in the specification. The alpha
CC globin gene sequence was obtained from Swiss.prot, no. AAP02023. The
CC mutation was then added to the sequence. The sequence was mutated by
CC polymerase chain reaction. The mutation introduced produced
CC oxygen exchange characteristics sufficiently close to natural
CC haemoglobin (Hb) to enable its use in a cell-free blood substitute.
CC The mutated gene encoding this protein can be used in a construct
CC designed for expression of pure, modified human Hb's in the
CC erythrocytes of non-human transgenic animals. The Hb's are non-
CC immunogenic so can be used without the need for blood typing. Also,
CC the transgenic Hb will be free of such viruses as HIV.
CC
XX
XX Sequence 146 AA:
SQ

```

Query Match 100.0%; Score 10; DB 13; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 LVVYPWTQRF 10
   |||
DB 32 LVVYPWTQRF 41

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RESULT 77
 ID AAR29610 standard; Protein; 146 AA.
 AC AAR29610;
 XX
 DT 15-JAN-1993 (first entry)

```

XX
XX Mutant human beta-globin 3.
DE
XX
XX Oxygen affinity; oxygen exchange; erythrocytes; HIV.
KM
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH misc_difference 102 /*tag= a
FT /label= beta_102_Asn_to_Thr
FT
XX
XX W09211283-A.
PN
XX
XX 09-JUL-1992.
PD
XX
XX 20-DEC-1991; 91WO-US09624.
PF
XX
XX 20-DEC-1990; 90US-0630825.
PR
XX
XX (UYAL-) UNIV ALABAMA RES FOUND.
PA
XX
XX McCune SL, Townes TM.
PI
XX
XX WPI; 1992-250026/30.
DR
XX N-PSDB; AAQ26428.
DR
XX
XX Transgenic, crosslinked polymeric human haemoglobin - useful as a
PT cell-free blood substitute
PT
XX
XX Disclosure; Page 13; 42pp; English.
XX
XX This sequence was not disclosed in the specification. The alpha
CC globin gene sequence was obtained from Swiss.prot, no. AAP02023. The
CC mutation was then added to the sequence. The sequence was mutated by
CC polymerase chain reaction. The mutation introduced lowered the
CC molecules oxygen affinity. This globin molecule has oxygen exchange
CC characteristics sufficiently close to natural haemoglobin (Hb) to
CC enable its use in a cell-free blood substitute.
CC The mutated gene encoding this protein can be used in a construct
CC designed for expression of pure, modified human Hb's in the
CC erythrocytes of non-human transgenic animals. The Hb's are non-
CC immunogenic so can be used without the need for blood typing. Also,
CC the transgenic Hb will be free of such viruses as HIV.
CC
XX
XX Sequence 146 AA:
SQ

```

Query Match 100.0%; Score 10; DB 13; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 LVVYPWTQRF 10
   |||
DB 32 LVVYPWTQRF 41

```

RESULT 78
 ID AAR30527 standard; protein; 146 AA.
 AC AAR30527;
 XX
 DT 13-MAY-1993 (first entry)
 XX
 XX Agenog beta globin.
 DE
 XX Globin; haemoglobin; Hb; affinity; oxygen; delivery; stroke;
 KM myocardial infarction; diabetes; tumour; x-ray treatment; burns;
 KW free radical; lesion.
 XX
 OS Homo sapiens.
 XX

```

EH Key Location/Qualifiers
FT Misc-difference 90
PT /Label- E90K
XX
XX US5173426-A.
XX
XX 22-DEC-1992.
XX
XX 06-OCT-1989; 89US-0417949.
XX
XX 06-OCT-1989; 89US-0417949.
XX
XX (UYYA ) UNIV YALE.
XX
XX Baserga SJ, Fischer JJ;
XX
XX WPI; 1993-017570/02.
XX
XX New polynucleotide(s) coding for mutant globin chains - form
PT haemoglobin with reduced oxygen affinity, useful e.g. for
PT increasing oxygenation of tumour cells
XX
XX PS Disclosure: Column 7; 11pp; English.
XX
XX The sequences given in AAR30527-33 represent mutant globin molecules
CC which when part of a haemoglobin (Hb) molecule, produces a mutant Hb
CC with a lower affinity for oxygen than normal Hb. The oxygen
CC affinity of the mutant Hb's being characterised by P50 of 30 Torr to
CC 3 atmos. and/or Hill coefficient of 2.5-1. The mutant Hb are useful
CC for increasing oxygen delivery to tissue in patients suffering from
CC myocardial infarction, stroke, diabetes etc. They may also be used
CC to make tumours more susceptible to x-ray treatment by combining
CC with free radicals and fixing the lesion in the cell. These Hb may
CC be used replace the Hb in an entire bloodstream and for treating
CC burns patients.
XX
XX SO Sequence 146 AA:

Query Match 100.0%; Score 10; DB 14; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
DB 32 LVVYPWTORE 41

RESULT 79
AAR30528
ID AAR30528 standard; protein; 146 AA.
XX
XX AAR30528;
XX
XX 13-MAY-1993 (first entry)
XX
XX E90G beta globin.
XX
XX Globin; haemoglobin; Hb; affinity; oxygen; delivery; stroke;
KW myocardial infarction; diabetes; tumour; x-ray treatment; burns;
KW free radical; lesion.
XX
XX Homo sapiens.
XX
XX OS
XX
XX Key Location/Qualifiers
FT Misc-difference 90
FT /Label- E90G
XX
XX US5173426-A.
XX
XX 22-DEC-1992.
XX
XX 06-OCT-1989; 89US-0417949.
XX
XX

```

```

XX
XX 06-OCT-1989; 89US-0417949.
XX
XX (UYYA ) UNIV YALE.
XX
XX Baserga SJ, Fischer JJ;
XX
XX WPI; 1993-017570/02.
XX
XX New polynucleotide(s) coding for mutant globin chains - form
PT haemoglobin with reduced oxygen affinity, useful e.g. for
PT increasing oxygenation of tumour cells
XX
XX PS Disclosure: Column 7; 11pp; English.
XX
XX The sequences given in AAR30527-33 represent mutant globin molecules
CC which when part of a haemoglobin (Hb) molecule, produces a mutant Hb
CC with a lower affinity for oxygen than normal Hb. The oxygen
CC affinity of the mutant Hb's being characterised by P50 of 30 Torr to
CC 3 atmos. and/or Hill coefficient of 2.5-1. The mutant Hb are useful
CC for increasing oxygen delivery to tissue in patients suffering from
CC myocardial infarction, stroke, diabetes etc. They may also be used
CC to make tumours more susceptible to x-ray treatment by combining
CC with free radicals and fixing the lesion in the cell. These Hb may
CC be used replace the Hb in an entire bloodstream and for treating
CC burns patients.
XX
XX SO Sequence 146 AA:

Query Match 100.0%; Score 10; DB 14; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
DB 32 LVVYPWTORE 41

RESULT 80
AAR30529
ID AAR30529 standard; protein; 146 AA.
XX
XX AAR30529;
XX
XX 13-MAY-1993 (first entry)
XX
XX Yoshizuka beta globin.
XX
XX Globin; haemoglobin; Hb; affinity; oxygen; delivery; stroke;
KW myocardial infarction; diabetes; tumour; x-ray treatment; burns;
KW free radical; lesion.
XX
XX Homo sapiens.
XX
XX OS
XX
XX Key Location/Qualifiers
FT Misc-difference 108
FT /Label- N108D
XX
XX US5173426-A.
XX
XX 22-DEC-1992.
XX
XX 06-OCT-1989; 89US-0417949.
XX
XX 06-OCT-1989; 89US-0417949.
XX
XX (UYYA ) UNIV YALE.
XX
XX Baserga SJ, Fischer JJ;
XX
XX WPI; 1993-017570/02.
XX

```

PT New polynucleotide(s) coding for mutant globin chains - form
 PT haemoglobin with reduced oxygen affinity, useful e.g. for
 PT increasing oxygenation of tumour cells
 XX
 PS Disclosure: Column 7; 11pp; English.
 CC The sequences given in AAR30527-33 represent mutant globin molecules
 CC which when part of a haemoglobin (Hb) molecule, produces a mutant Hb
 CC with a lower affinity for oxygen than normal Hb. The oxygen
 CC affinity of the mutant Hb's being characterised by P50 of 30 Torr to
 CC 3 atmos. and/or Hill coefficient of 2.5-1. The mutant Hb are useful
 CC for increasing oxygen delivery to tissue in patients suffering from
 CC myocardial infarction, stroke, diabetes etc. They may also be used
 CC to make tumours more susceptible to x-ray treatment by combining
 CC with free radicals and fixing the lesion in the cell. These Hb may
 CC be used replace the Hb in an entire bloodstream and for treating
 CC burns patients.
 CC
 SQ Sequence 146 AA:
 XX
 XX

Query Match 100.0%; Score 10; DB 14; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10
 |||||
 DB 32 LVVYPTQRF 41

RESULT 81
 AAR30530
 ID AAR30530 standard; protein; 146 AA.
 XX
 AC AAR30530;
 XX
 DT 13-MAY-1993 (first entry)
 XX
 DE Kansas beta globin.
 XX
 KW Globin; haemoglobin; Hb; affinity; oxygen; delivery; stroke;
 KW myocardial infarction; diabetes; tumour; x-ray treatment; burns;
 KW free radical; lesion.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 102
 FT /label= N102F
 XX
 US5173426-A.
 XX
 PN 22-DEC-1992.
 XX
 PD 06-OCT-1989; 89US-0417949.
 XX
 PF 06-OCT-1989; 89US-0417949.
 XX
 PR 06-OCT-1989; 89US-0417949.
 XX
 PT (UYVA) UNIV YALE.
 XX
 PA
 XX
 PI Baserga SJ, Fischer JJ;
 XX
 DR WPI; 1993-017570/02.
 XX
 CC The sequences given in AAR30527-33 represent mutant globin molecules
 CC which when part of a haemoglobin (Hb) molecule, produces a mutant Hb
 CC with a lower affinity for oxygen than normal Hb. The oxygen
 CC affinity of the mutant Hb's being characterised by P50 of 30 Torr to
 CC 3 atmos. and/or Hill coefficient of 2.5-1. The mutant Hb are useful
 CC for increasing oxygen delivery to tissue in patients suffering from
 CC myocardial infarction, stroke, diabetes etc. They may also be used
 CC to make tumours more susceptible to x-ray treatment by combining
 CC with free radicals and fixing the lesion in the cell. These Hb may
 CC be used replace the Hb in an entire bloodstream and for treating
 CC burns patients.
 CC

CC affinity of the mutant Hb's being characterised by P50 of 30 Torr to
 CC 3 atmos. and/or Hill coefficient of 2.5-1. The mutant Hb are useful
 CC for increasing oxygen delivery to tissue in patients suffering from
 CC myocardial infarction, stroke, diabetes etc. They may also be used
 CC to make tumours more susceptible to x-ray treatment by combining
 CC with free radicals and fixing the lesion in the cell. These Hb may
 CC be used replace the Hb in an entire bloodstream and for treating
 CC burns patients.
 CC
 SQ Sequence 146 AA:
 XX
 XX

Query Match 100.0%; Score 10; DB 14; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10
 |||||
 DB 32 LVVYPTQRF 41

RESULT 82
 AAR30531
 ID AAR30531 standard; protein; 146 AA.
 XX
 AC AAR30531;
 XX
 DT 13-MAY-1993 (first entry)
 XX
 DE Beth israel beta globin.
 XX
 KW Globin; haemoglobin; Hb; affinity; oxygen; delivery; stroke;
 KW myocardial infarction; diabetes; tumour; x-ray treatment; burns;
 KW free radical; lesion.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 102
 FT /label= N102S
 XX
 US5173426-A.
 XX
 PN 22-DEC-1992.
 XX
 PD 06-OCT-1989; 89US-0417949.
 XX
 PF 06-OCT-1989; 89US-0417949.
 XX
 PR 06-OCT-1989; 89US-0417949.
 XX
 PT (UYVA) UNIV YALE.
 XX
 PA
 XX
 PI Baserga SJ, Fischer JJ;
 XX
 DR WPI; 1993-017570/02.
 XX
 CC The sequences given in AAR30527-33 represent mutant globin molecules
 CC which when part of a haemoglobin (Hb) molecule, produces a mutant Hb
 CC with a lower affinity for oxygen than normal Hb. The oxygen
 CC affinity of the mutant Hb's being characterised by P50 of 30 Torr to
 CC 3 atmos. and/or Hill coefficient of 2.5-1. The mutant Hb are useful
 CC for increasing oxygen delivery to tissue in patients suffering from
 CC myocardial infarction, stroke, diabetes etc. They may also be used
 CC to make tumours more susceptible to x-ray treatment by combining
 CC with free radicals and fixing the lesion in the cell. These Hb may
 CC be used replace the Hb in an entire bloodstream and for treating
 CC burns patients.
 CC

SQ Sequence 146 AA:

Query Match 100.0%; Score 10; DB 14; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORF 10
 |||||
 DB 32 LVVYPWTORF 41

RESULT 83

ID AAR30532 standard; protein; 146 AA.
 AC AAR30532;

DT 13-MAY-1993 (first entry)
 DE Root effect beta globin.

KW Globin; haemoglobin; Hb; affinity; oxygen; delivery; stroke;
 KW myocardial infarction; diabetes; tumour; X-ray treatment; burns;
 KW free radical; lesion.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Misc-difference 90 /Label- E90V

FT Misc-difference 91 /Label- L91M
 FT Misc-difference 93 /Label- C93S

FT Misc-difference 94 /Label- D90E
 FT

XX US5173426-A.
 PN

XX 22-DEC-1992.
 PD

XX 06-OCT-1989; 89US-0417949.
 PP

XX 06-OCT-1989; 89US-0417949.
 PR

XX (UYVA) UNIV YALE.
 PA

XX Baserga SJ, Fischer JU;
 PI

XX WPI; 1993-017570/02.
 DR

XX New polynucleotide(s) coding for mutant globin chains - form
 PT haemoglobin with reduced oxygen affinity, useful e.g. for
 PT increasing oxygenation of tumour cells
 PS

XX Disclosure; Column 7; 11pp; English.
 PS

XX The sequences given in AAR30527-33 represent mutant globin molecules
 CC which when part of a haemoglobin (Hb) molecule, produces a mutant Hb
 CC with a lower affinity for oxygen than normal Hb. The oxygen
 CC affinity of the mutant Hb's being characterised by P50 of 30 Torr to
 CC 3 atmos. and/or Hill coefficient of 2.5-1. The mutant Hb are useful
 CC for increasing oxygen delivery to tissue in patients suffering from
 CC myocardial infarction, stroke, diabetes etc. They may also be used
 CC to make tumours more susceptible to X-ray treatment by combining
 CC with free radicals and fixing the lesion in the cell. These Hb may
 CC be used to replace the Hb in an entire bloodstream and for treating
 CC burns patients.
 CC

SQ Sequence 146 AA:

Query Match 100.0%; Score 10; DB 14; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORF 10
 |||||
 DB 32 LVVYPWTORF 41

RESULT 84

ID AAR32989 standard; Protein; 146 AA.
 AC AAR32989;

DT 17-JUN-1993 (first entry)
 DE Human beta Haemoglobin and petunia EPSP synthase transit peptide.

KW Recombinant products; commercial production; fermentation;
 KW biosynthesis; natural products; recombinant proteins;
 KW product expression; protein expression; expressed proteins.

OS Chimaeric - Homo sapiens.
 OS Chimaeric - Petunia sp.

XX WO9303161-A.
 PN

XX 18-FEB-1993.
 PD

XX 31-JUL-1992; 92WO-US06359.
 PF

XX 01-AUG-1991; 91US-0739143.
 PR

XX (DAMS/) DAWSON W O.
 PA (DONS/) DONSON J.
 PA (GARG/) GARGER S J.
 PA (GRAN/) GRANTHAM G L.
 PA (GRIL/) GRILLE L K.
 PA (TURP/) TURPEN A M.
 PA (TURP/) TURPEN T H.

XX Dawson WO, Donson J, Garger SJ, GrantHAM GL, Grille LK;
 PI TurpenAM, Turpen TH;
 XX

XX WPI; 1993-076518/09.
 DR N-PSDB; Q376810.
 DR

XX Recombinant plant viral nucleic acids - used to express a prod.,
 PT e.g. antibody or IL-1 in a plant
 PT

XX Example 4; Page 105; 30pp; English.
 PS

XX This sequence is human beta-haemoglobin with petunia EPSP synthase
 CC transit peptide. The coding sequence was inserted into recombinant plant
 CC viral nucleic acid which was then used to express a recombinant product
 CC (in this case human beta-Hb) in a plant. The plant viral sequence
 CC may be from tobacco mosaic, cucumber green mottle, cowpea mosaic, brome
 CC mosaic, broad bean mottle, rice necrosis, geminiviruses, tomato golden
 CC mosaic, Cassava latent and maize streak viruses.
 CC

SQ Sequence 146 AA:

Query Match 100.0%; Score 10; DB 14; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORF 10
 |||||
 DB 32 LVVYPWTORF 41

RESULT 85
 AAR39716
 ID AAR39716 standard; Protein; 146 AA.
 XX
 AC AAR39716;
 XX
 DT 08-SEP-1993 (first entry)
 XX
 DE Human embryonic epsilon haemoglobin.
 XX
 KW Embryonic; zeta; epsilon; fetal; gamma; adult; delta; alpha; beta;
 KW haemoglobin; methionine aminopeptidase; oxygen affinity; HbF Chlco;
 KW post-translational modification; HbA Deer Lodge; HbA Abruzzo; Yeast;
 KW Hb Portland Titusville; HbA Motown/Hacettepe; alkaline stability;
 KW HbA McKees Rock; transformation; Hb Bovill; blood substitute solution;
 KW globin; physiological; oxygen carrier; plasma expander.
 XX
 OS Homo sapiens.
 XX
 PN MO9308831-A.
 XX
 PD 13-MAY-1993.
 XX
 PF 30-OCT-1991; 91WO-US08108.
 XX
 PR 30-OCT-1991; 91WO-US08108.
 XX
 PA (STRO-) STROHTECH INC.
 XX
 PI Bajwa W, De Angelo J, Motwani NM;
 XX
 DR WPI: 1993-167394/20.
 DR N-PSDB; AAQ46961.
 XX
 PT New haemoglobin variants bind reversibly to oxygen - useful as
 PT physiological oxygen carriers (e.g. in blood substitutes) and as
 PT plasma expanders
 XX
 PS Disclosure; Fig 1b; 211pp; English.
 XX
 CC The sequences given in AAR39715-20 represent embryonic zeta, embryonic
 CC epsilon, fetal gamma, adult delta, adult alpha and adult beta haemo-
 CC globins. The AUG start codon and the corresponding amino terminal
 CC Met are removed by methionine aminopeptidase in a post-translational
 CC modification. Further modifications of these protein sequences may
 CC produce globins that may have lower oxygen affinity, eg. HbF Chlco,
 CC Hb Portland Titusville and Hb Bovill (see also AAR39721-23). Higher
 CC oxygen affinity, eg. HbA Deer Lodge, HbA Abruzzo and HbA McKees Rock
 CC (see also AAR39724-6), alkaline stable variants, eg. HbA
 CC Motown/Hacettepe (see also AAR39727) or variants which have a lower
 CC oxygen affinity and are stable in alkali (see also AAR39728). The DNA
 CC sequences encoding these globin variants may be used to transform yeasts
 CC such that they produce the globins. The variant globins may be used in
 CC applications which require physiological oxygen carriers, such as in
 CC blood substitute solutions, or as plasma expanders.
 XX
 SQ Sequence 146 AA;
 XX

Query Match 100.0%; Score 10; DB 14; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORF 10
 Db 32 LVVYPWTGRF 41

RESULT 86
 AAR39717
 ID AAR39717 standard; Protein; 146 AA.
 XX
 AC AAR39717;
 XX

XX
 DT 08-SEP-1993 (first entry)
 XX
 DE Human fetal gamma haemoglobin.
 XX
 KW Embryonic; zeta; epsilon; fetal; gamma; adult; delta; alpha; beta;
 KW haemoglobin; methionine aminopeptidase; oxygen affinity; HbF Chlco;
 KW post-translational modification; HbA Deer Lodge; HbA Abruzzo; Yeast;
 KW Hb Portland Titusville; HbA Motown/Hacettepe; alkaline stability;
 KW HbA McKees Rock; transformation; Hb Bovill; blood substitute solution;
 KW globin; physiological; oxygen carrier; plasma expander.
 XX
 OS Homo sapiens.
 XX
 PN MO9308831-A.
 XX
 PD 13-MAY-1993.
 XX
 PF 30-OCT-1991; 91WO-US08108.
 XX
 PR 30-OCT-1991; 91WO-US08108.
 XX
 PA (STRO-) STROHTECH INC.
 XX
 PI Bajwa W, De Angelo J, Motwani NM;
 XX
 DR WPI: 1993-167394/20.
 DR N-PSDB; AAQ46962.
 XX
 PT New haemoglobin variants bind reversibly to oxygen - useful as
 PT physiological oxygen carriers (e.g. in blood substitutes) and as
 PT plasma expanders
 XX
 PS Disclosure; Fig 1c; 211pp; English.
 XX
 CC The sequences given in AAR39715-20 represent embryonic zeta, embryonic
 CC epsilon, fetal gamma, adult delta, adult alpha and adult beta haemo-
 CC globins. The AUG start codon and the corresponding amino terminal
 CC Met are removed by methionine aminopeptidase in a post-translational
 CC modification. Further modifications of these protein sequences may
 CC produce globins that may have lower oxygen affinity, eg. HbF Chlco,
 CC Hb Portland Titusville and Hb Bovill (see also AAR39721-23). Higher
 CC oxygen affinity, eg. HbA Deer Lodge, HbA Abruzzo and HbA McKees Rock
 CC (see also AAR39724-6), alkaline stable variants, eg. HbA
 CC Motown/Hacettepe (see also AAR39727) or variants which have a lower
 CC oxygen affinity and are stable in alkali (see also AAR39728). The DNA
 CC sequences encoding these globin variants may be used to transform yeasts
 CC such that they produce the globins. The variant globins may be used in
 CC applications which require physiological oxygen carriers, such as in
 CC blood substitute solutions, or as plasma expanders.
 XX
 SQ Sequence 146 AA;
 XX

Query Match 100.0%; Score 10; DB 14; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORF 10
 Db 32 LVVYPWTGRF 41

RESULT 87
 AAR39718
 ID AAR39718 standard; Protein; 146 AA.
 XX
 AC AAR39718;
 XX
 DT 08-SEP-1993 (first entry)
 XX
 DE Human adult delta haemoglobin.
 XX

KM Embryonic; zeta; epsilon; fetal; gamma; adult; delta; alpha; beta;
 KM haemoglobin; methionine aminopeptidase; oxygen affinity; HbF Chico;
 KM post-translational modification; HbA Deer Lodge; HbA Abruzzo; yeast;
 KM Hb Portland Titusville; HbA Motown/Hacettepe; alkaline stability;
 KM HbA McKees Rock; transformation; Hb Bovitt; blood substitute solution;
 KM globin; physiological; oxygen carrier; plasma expander.
 OS Homo sapiens.
 XX WO9308831-A.
 XX 13-MAY-1993.
 XX 30-OCT-1991; 91WO-US08108.
 XX 30-OCT-1991; 91WO-US08108.
 XX 30-OCT-1991; 91WO-US08108.
 XX (STRO-) STROHTECH INC.
 XX Bajwa W, De Angelo J, Motwani NM;
 XX WPI: 1993-167394/20.
 XX N-PSDB; AAQ46963.
 PT New haemoglobin variants bind reversibly to oxygen - useful as
 PT physiological oxygen carriers (e.g. in blood substitutes) and as
 PT plasma expanders
 PS Disclosure: Fig 1D; 21pp; English.
 XX The sequences given in AAR39715-20 represent embryonic zeta, embryonic
 CC epsilon, fetal gamma, adult delta, adult alpha and adult beta haemo-
 CC globins. The AUG start codon and the corresponding amino terminal
 CC Met are removed by methionine aminopeptidase in a post-translational
 CC modification. Further modifications of these protein sequences may
 CC produce globins that may have lower oxygen affinity, eg. HbF Chico,
 CC Hb Portland Titusville and Hb Bovitt (see also AAR39721-23), higher
 CC oxygen affinity, eg. HbA Deer Lodge, HbA Abruzzo and HbA McKees Rock
 CC (see also AAR39724-6), alkaline stable variants, eg. HbA
 CC Motown/Hacettepe (see also AAR39727) or variants which have a lower
 CC oxygen affinity and are stable in alkali (see also AAR39728). The DNA
 CC sequences encoding these globin variants may be used to transform yeasts
 CC such that they produce the globins. The variant globins may be used in
 CC applications which require physiological oxygen carriers, such as in
 CC blood substitute solutions, or as plasma expanders.
 CC
 CC Sequence 146 AA:
 SQ
 Query Match 100.0%; Score 10; DB 14; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVVYPWTORE 10
 DB 32 LVVYPWTGTF 41
 RESULT 88
 AAR39720
 ID AAR39720 standard; Protein: 146 AA.
 XX AAR39720;
 XX 08-SEP-1993 (first entry)
 XX Human beta alpha haemoglobin.
 DE Embryonic; zeta; epsilon; fetal; gamma; adult; delta; alpha; beta;
 KM haemoglobin; methionine aminopeptidase; oxygen affinity; HbF Chico;
 KM post-translational modification; HbA Deer Lodge; HbA Abruzzo; yeast;
 KM Hb Portland Titusville; HbA Motown/Hacettepe; alkaline stability;
 KM HbA McKees Rock; transformation; Hb Bovitt; blood substitute solution;

KM globin; physiological; oxygen carrier; plasma expander.
 XX Homo sapiens.
 OS WO9308831-A.
 XX 13-MAY-1993.
 XX 30-OCT-1991; 91WO-US08108.
 XX 30-OCT-1991; 91WO-US08108.
 XX 30-OCT-1991; 91WO-US08108.
 XX (STRO-) STROHTECH INC.
 XX Bajwa W, De Angelo J, Motwani NM;
 XX WPI: 1993-167394/20.
 XX N-PSDB; AAQ46965.
 DR New haemoglobin variants bind reversibly to oxygen - useful as
 DR physiological oxygen carriers (e.g. in blood substitutes) and as
 DR plasma expanders
 PS Disclosure: Fig 1F; 21pp; English.
 XX The sequences given in AAR39715-20 represent embryonic zeta, embryonic
 CC epsilon, fetal gamma, adult delta, adult alpha and adult beta haemo-
 CC globins. The AUG start codon and the corresponding amino terminal
 CC Met are removed by methionine aminopeptidase in a post-translational
 CC modification. Further modifications of these protein sequences may
 CC produce globins that may have lower oxygen affinity, eg. HbF Chico,
 CC Hb Portland Titusville and Hb Bovitt (see also AAR39721-23), higher
 CC oxygen affinity, eg. HbA Deer Lodge, HbA Abruzzo and HbA McKees Rock
 CC (see also AAR39724-6), alkaline stable variants, eg. HbA
 CC Motown/Hacettepe (see also AAR39727) or variants which have a lower
 CC oxygen affinity and are stable in alkali (see also AAR39728). The DNA
 CC sequences encoding these globin variants may be used to transform yeasts
 CC such that they produce the globins. The variant globins may be used in
 CC applications which require physiological oxygen carriers, such as in
 CC blood substitute solutions, or as plasma expanders.
 CC
 CC Sequence 146 AA:
 SQ
 Query Match 100.0%; Score 10; DB 14; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVVYPWTORE 10
 DB 32 LVVYPWTGTF 41
 RESULT 89
 AAR39721
 ID AAR39721 standard; Protein: 146 AA.
 XX AAR39721;
 XX 08-SEP-1993 (first entry)
 XX HbF Chico haemoglobin.
 DE Embryonic; zeta; epsilon; fetal; gamma; adult; delta; alpha; beta;
 KM haemoglobin; methionine aminopeptidase; oxygen affinity; HbF Chico;
 KM post-translational modification; HbA Deer Lodge; HbA Abruzzo; yeast;
 KM Hb Portland Titusville; HbA Motown/Hacettepe; alkaline stability;
 KM HbA McKees Rock; transformation; Hb Bovitt; blood substitute solution;
 KM globin; physiological; oxygen carrier; plasma expander.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers

```

FT  Misc-difference 66
XX  /label= K66T
XX  WO9308831-A.
XX
XX  13-MAY-1993.
XX
XX  30-OCT-1991; 91WO-US08108.
XX
XX  30-OCT-1991; 91WO-US08108.
XX
XX  30-OCT-1991; 91WO-US08108.
XX
XX  (STRO-) STROHTECH INC.
XX
XX  Bajwa W, De Angelo J, Motwani NM;
XX  WPI; 1993-167394/20.
XX
XX  New haemoglobin variants bind reversibly to oxygen - useful as
XX  physiological oxygen carriers (e.g. in blood substitutes) and as
XX  plasma expanders
XX
XX  Disclosure; Page 13; 211pp; English.
XX
XX  The sequences given in AAR39721-28 represent variant haemoglobins
XX  derived from embryonic zeta, embryonic epsilon, fetal gamma, adult
XX  delta, adult alpha and adult beta haemoglobins. The variants HbF
XX  Chico, Hb Portland Titusville and Hb Bovill have lower oxygen affinity,
XX  HbA Deer Lodge, HbA Abruzzo and HbA McKees Rock have higher oxygen
XX  affinity. HbA Motown/Hacettepe is an alkaline stable variant compared
XX  to the wild-type molecules, and a further variant was produced which
XX  had a lower oxygen affinity and was stable in alkali. The DNA
XX  sequences encoding these globin variants may be used to transform
XX  yeasts such that they produce the globins. The variant globins may
XX  be used in applications which require physiological oxygen carriers,
XX  such as in blood substitute solutions, or as plasma expanders.
XX
XX  Sequence 146 AA;
XX
Query Match 100.0%; Score 10; DB 14; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LVVYPWTORF 10
Db 32 LVVYPWTCRF 41

```

RESULT 90

AAR39724 standard; Protein: 146 AA.

```

XX  AAR39724;
XX
XX  08-SEP-1993 (first entry)
XX
XX  HbA Deer Lodge.
XX
XX  Embryonic; zeta; epsilon; fetal; gamma; adult; delta; alpha; beta;
XX  haemoglobin; methionine aminopeptidase; oxygen affinity; HbF Chico;
XX  post-translational modification; HbA Deer Lodge; HbA Abruzzo; yeast;
XX  Hb Portland Titusville; HbA Motown/Hacettepe; alkaline stability;
XX  HbA McKees Rock; transformation; Hb Bovill; blood substitute solution;
XX  globin; physiological; oxygen carrier; plasma expander.
XX
XX  Homo sapiens.
XX
XX  Key Location/Qualifiers
XX  Misc-difference 2 /label= H2R
XX
XX  WO9308831-A.
XX

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PD  13-MAY-1993.
XX
XX  30-OCT-1991; 91WO-US08108.
XX
XX  30-OCT-1991; 91WO-US08108.
XX
XX  (STRO-) STROHTECH INC.
XX
XX  Bajwa W, De Angelo J, Motwani NM;
XX  WPI; 1993-167394/20.
XX
XX  New haemoglobin variants bind reversibly to oxygen - useful as
XX  physiological oxygen carriers (e.g. in blood substitutes) and as
XX  plasma expanders
XX
XX  Disclosure; Page 13; 211pp; English.
XX
XX  The sequences given in AAR39721-28 represent variant haemoglobins
XX  derived from embryonic zeta, embryonic epsilon, fetal gamma, adult
XX  delta, adult alpha and adult beta haemoglobins. The variants HbF
XX  Chico, Hb Portland Titusville and Hb Bovill have lower oxygen affinity,
XX  HbA Deer Lodge, HbA Abruzzo and HbA McKees Rock have higher oxygen
XX  affinity. HbA Motown/Hacettepe is an alkaline stable variant compared
XX  to the wild-type molecules, and a further variant was produced which
XX  had a lower oxygen affinity and was stable in alkali. The DNA
XX  sequences encoding these globin variants may be used to transform
XX  yeasts such that they produce the globins. The variant globins may
XX  be used in applications which require physiological oxygen carriers,
XX  such as in blood substitute solutions, or as plasma expanders.
XX
XX  Sequence 146 AA;
XX
Query Match 100.0%; Score 10; DB 14; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LVVYPWTORF 10
Db 32 LVVYPWTCRF 41

```

RESULT 91

AAR39725 standard; Protein: 146 AA.

```

XX  AAR39725;
XX
XX  08-SEP-1993 (first entry)
XX
XX  HbA Abruzzo.
XX
XX  Embryonic; zeta; epsilon; fetal; gamma; adult; delta; alpha; beta;
XX  haemoglobin; methionine aminopeptidase; oxygen affinity; HbF Chico;
XX  post-translational modification; HbA Deer Lodge; HbA Abruzzo; yeast;
XX  Hb Portland Titusville; HbA Motown/Hacettepe; alkaline stability;
XX  HbA McKees Rock; transformation; Hb Bovill; blood substitute solution;
XX  globin; physiological; oxygen carrier; plasma expander.
XX
XX  Homo sapiens.
XX
XX  Key Location/Qualifiers
XX  Misc-difference 143 /label= H143R
XX
XX  WO9308831-A.
XX
XX  13-MAY-1993.
XX
XX  30-OCT-1991; 91WO-US08108.
XX
XX  30-OCT-1991; 91WO-US08108.
XX

```

XX (STRO-) STROTECH INC.
 XX Bajwa W, De Angelo J, Motwani NM;
 PI WPI; 1993-167394/20.
 DR
 XX New haemoglobin variants bind reversibly to oxygen - useful as
 PT physiological oxygen carriers (e.g. in blood substitutes) and as
 PT plasma expanders
 XX
 PS Disclosure; Page 13; 21pp; English.
 XX
 CC The sequences given in AAR39721-28 represent variant haemoglobins
 CC derived from embryonic zeta, embryonic epsilon, fetal gamma, adult
 CC delta, adult alpha and adult beta haemoglobins. The variants Hbp
 CC Chico, Hb Portland Titusville and Hb Bovill have lower oxygen affinity,
 CC HbA Deer Lodge, HbA Arruzzo and HbA McKees Rock have higher oxygen
 CC affinity, HbA Motown/Alacetepe is an alkaline stable variant compared
 CC to the wild-type molecules, and a further variant was produced which
 CC had a lower oxygen affinity and was stable in alkali. The DNA
 CC sequences encoding these globin variants may be used to transform
 CC yeasts such that they produce the globins. The variant globins may
 CC be used in applications which require physiological oxygen carriers,
 CC such as in blood substitute solutions, or as plasma expanders.
 CC
 XX
 SQ Sequence 146 AA:

Query Match 100.0%; Score 10; DB 14; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPMTORF 10
 |||||
 Db 32 LVVYPMTCRF 41

RESULT 92
 AAR39458
 ID AAR39458 standard; Protein; 146 AA.
 XX
 AC AAR39458;
 XX
 DT 09-SEP-1993 (first entry)
 XX
 DE Des-Val beta globin.
 XX
 KW PSEG1.1E4; multimeric haemoglobin; pseudotetramer;
 KW crosslinking cysteine; blood.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 2..4 "potential sites for Xaa -> Cys mutation
 FT to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 6 "potential site for Xaa -> Cys mutation
 FT to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 9 "potential site for Xaa -> Cys mutation
 FT to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 12..13 "potential sites for Xaa -> Cys mutation
 FT to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 16..22 "potential sites for Xaa -> Cys mutation
 FT to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 43..44 "potential sites for Xaa -> Cys mutation
 FT to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 47

FT /note- "potential site for Xaa -> Cys mutation
 FT to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 49..50 "potential sites for Xaa -> Cys mutation
 FT to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 52..53 "potential sites for Xaa -> Cys mutation
 FT to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 59 "potential site for Xaa -> Cys mutation
 FT to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 61..62 "potential sites for Xaa -> Cys mutation
 FT to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 65..66 "potential sites for Xaa -> Cys mutation
 FT to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 72..73 "potential sites for Xaa -> Cys mutation
 FT to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 76..80 "potential sites for Xaa -> Cys mutation
 FT to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 83 "potential site for Xaa -> Cys mutation
 FT to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 86..87 "potential sites for Xaa -> Cys mutation
 FT to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 90 "potential site for Xaa -> Cys mutation
 FT to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 95 "potential site for Xaa -> Cys mutation
 FT to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 116..117 "potential sites for Xaa -> Cys mutation
 FT to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 120..121 "potential sites for Xaa -> Cys mutation
 FT to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 123 "potential site for Xaa -> Cys mutation
 FT to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 70 "potential site for Xaa -> Cys mutation
 FT to provide a crosslinkable site; see CC"
 FT
 FT Misc-difference 11..40 "candidate sites for mutation to block
 FT haptoglobin binding"
 FT
 FT Misc-difference 131..146 "candidate sites for mutation to block
 FT haptoglobin binding"
 FT
 FT W09309143-A.
 PN
 PD 13-MAY-1993.
 XX
 XX 06-NOV-1992; 92WO-US09752.
 XX
 XX 08-NOV-1991; 91US-0789179.
 XX
 XX (SOMA-) SOMATOGEN INC.
 XX
 XX Anderson DC, Mathews AJ, Stetler GL;
 XX WPI; 1993-167626/20.
 DR N-PSDB; AA042395.
 XX
 XX Non-natural multimeric haemoglobin-like protein - based on
 PT pseudo-tetramer contg. pseudo-dimer polypeptide with globin-like

PT domains, used to prolong haemoglobin half life and supplement
 PT oxygen carrying capacity of blood
 XX
 PS Disclosure: Fig 2; 161pp; English.
 CC The pref. synthetic gene for expression of (des-Val)-alpha-(gly)-
 CC alpha and des-Val beta globin is carried by PSGE1.184. The first
 CC alpha globin sequence begins with "Met-Leu", that is, it contains
 CC an artifactual methionine, omits the valine which is the normal
 CC first residue of mature alpha globin, and continues with the
 CC second residue, leucine. The second alpha globin sequence begins
 CC with "Val-Leu", immediately after the linker.
 CC The Xaa -> Cys mutations should be made asymmetrically, i.e., only
 CC one region of a di-alpha or di-beta gene, so only one crosslink is
 CC added per tetramer.
 CC
 XX Sequence 146 AA;
 SQ
 QY 1 LVVYPWTQRF 10
 |||||||||
 Db 32 LVVYPWTGRF 41
 Query Match 100.0%; Score 10; DB 14; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 93
 AAR42632
 ID AAR42632 standard; Protein; 146 AA.
 XX
 AC AAR42632;
 XX
 DT 26-APR-1994 (first entry)
 XX
 DE Natural beta-globin.
 XX
 KW Haemoglobin: alpha globin: beta globin: blood substitute;
 KW oxygen carrier: reversible oxygen fixation: chimeric gene;
 KW fusion protein.
 XX
 PN MO9319089-A.
 XX
 PD 30-SEP-1993.
 XX
 PF 18-MAR-1993; 93MO-FR00273.
 XX
 PR 18-MAR-1992; 92FR-0003224.
 XX
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PA (INMR) PASTEUR MERIEUX SERUMS & VACCINS.
 XX
 PI Edelman S, Pagnier RJ, Foyart C;
 XX
 DR WPI: 1993-320682/40.
 DR N-PSDB; AAQ49616.
 XX
 PT New synthetic tetrameric globin type oxygen transporter - with
 PT all chains identical and contg. haem, useful as blood substitute
 PT for transfusion
 XX
 PS Disclosure: Fig 2; 41pp; French.
 XX
 CC Chimeric alpha-beta globin molecules are claimed which, when
 CC associated together to reconstitute the alpha1-beta2 interface and
 CC incorporating haem, are suitable as blood substitutes. Pref. the
 CC chimeric chains contain amino acids 1-73 of beta globin at the
 CC N-terminus and amino acids 69 onwards of alpha-globin at the
 CC C-terminus. Alternatively, each chain may contain the N-terminus of
 CC an alpha chain with the C-terminus of a beta-chain, or all 4
 CC chains can be of the beta type. The tetramers are characterised by
 CC a lower oxygen affinity than natural haemoglobin.

XX
 SQ Sequence 146 AA;
 QY 1 LVVYPWTQRF 10
 |||||||||
 Db 32 LVVYPWTGRF 41
 Query Match 100.0%; Score 10; DB 14; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 94
 AAR55132
 ID AAR55132 standard; Protein; 146 AA.
 XX
 AC AAR55132;
 XX
 DT 12-JAN-1995 (first entry)
 XX
 DE Human beta haemoglobin.
 XX
 KW Virus: recombination; plant virus; alpha trichosanthin; phenoltype;
 KW alpha amylase; alpha haemoglobin; brome mosaic virus; gemini virus;
 KW rice necrosis virus tobamovirus; gene expression; chinese cucumber;
 KW beta haemoglobin.
 XX
 OS Homo sapiens.
 XX
 PN US5316931-A.
 XX
 PD 31-MAY-1994.
 XX
 PF 26-FEB-1988; 88US-0160766.
 XX
 PR 26-FEB-1988; 88US-0160766.
 PR 15-JUL-1988; 88US-0160771.
 PR 17-FEB-1989; 88US-0219279.
 PR 05-MAY-1989; 89US-0310881.
 PR 08-JUN-1989; 89US-0347637.
 PR 22-OCT-1990; 90US-0363138.
 PR 16-JAN-1991; 90US-0600244.
 PR 26-JUL-1991; 91US-0641617.
 PR 01-AUG-1991; 91US-0737899.
 XX
 PA (BIOS-) BIOSOURCE GENETICS CORP.
 XX
 PI Dawson WO, Donson J, Garger SJ, Grantham GL, Grilli LK;
 PI Turpen AM, Turpen TH;
 XX
 DR WPI: 1994-176269/21.
 DR N-PSDB; AAQ65576.
 XX
 PT New recombinant plant viral nucleic acid - capable of systemic
 PT infection and stable expression of non-native nucleic acid in
 PT plant host
 XX
 PS Example 4; Columns 59-62; 44pp; English.
 XX
 CC The beta haemoglobin coding sequence was fused to a sequence
 CC encoding the petunia E5SP synthase transit peptide and inserted into
 CC a recombinant plant virus which can then be used to infect plants
 CC for the production of non-native products (in this case human
 CC beta-haemoglobin). Other genes which may be inserted into the
 CC virus are those which control a phenotypic trait, such as male
 CC sterility, or sequences encoding anti-sense RNA which can be useful
 CC to prevent the expression of undesired phenotypic traits. The
 CC recombinant virus is derived from a plus sense, single stranded
 CC virus selected from tobamovirus, brome mosaic virus, rice necrosis
 CC virus or a gemini virus.

SQ Sequence 146 AA:

Query Match 100.0%; Score 10; DB 15; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
|||||
Db 32 LVVYPWTQRF 41

RESULT 95

ID AAR44522 standard; Protein; 146 AA.

XX AAR44522;

XX 23-JUN-1994 (first entry)

DE Adult human beta-globin C112I.

KM Adult; pig; beta; globin; gene; regulatory region; promoter;
KM transgenic pig; human; alpha; haemoglobin; Hb; erythrocyte;
KW transfusion; human/pig; hybrid Hb.

XX Homo sapiens.

FH Key Location/Qualifiers

FT Misc-difference 112 /label= C112I

XX WO9325071-A.

XX 23-DEC-1993.

XX 11-JUN-1993; 93WO-US05629.

XX 12-JUN-1992; 92US-0897648.

XX 08-DEC-1992; 92US-0987890.

XX 15-MAR-1993; 93US-0030897.

XX (DNXD-) DNX CORP.

PI Holzman SH, Keller H, Kumar R, Logan JS, O' Donnell JK;

PI Parsons CT, Pilder SH, Pinkert CA, Sharma A, Swanson ME;

PI White SP;

PS Claim 15; : 117pp; English.

The sequences given in AAR44521-28 represent mutant versions of the adult human beta globin sequence. These sequences were not given in the specification but were generated using the known beta globin sequence. These sequences were used in the production of constructs which were used to produce the transgenic pigs of the invention. These constructs contain the pig beta globin promoter sequence operably linked to the human alpha or beta globin genes. Pigs containing these constructs express human haemoglobin (Hb) in their erythrocytes and are healthy, suffering no deleterious side effects as a result of heterologous Hb production. They can be used as an efficient and economical source of human Hb that can be used for transfusion and other medical applications. Also, a human/pig hybrid Hb can be produced which exhibits a p50 that is higher than that of native human or pig Hb.

XX Sequence 146 AA:

Query Match 100.0%; Score 10; DB 15; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
|||||
Db 32 LVVYPWTQRF 41

RESULT 95

ID AAR44523 standard; Protein; 146 AA.

XX AAR44523;

XX 23-JUN-1994 (first entry)

DE Adult human beta-globin A115V.

KM Adult; pig; beta; globin; gene; regulatory region; promoter;
KM transgenic pig; human; alpha; haemoglobin; Hb; erythrocyte;
KW transfusion; human/pig; hybrid Hb.

XX Homo sapiens.

FH Key Location/Qualifiers

FT Misc-difference 115 /label= A115V

XX WO9325071-A.

XX 23-DEC-1993.

XX 11-JUN-1993; 93WO-US05629.

XX 12-JUN-1992; 92US-0897648.

XX 08-DEC-1992; 92US-0987890.

XX 15-MAR-1993; 93US-0030897.

XX (DNXD-) DNX CORP.

PI Holzman SH, Keller H, Kumar R, Logan JS, O' Donnell JK;

PI Parsons CT, Pilder SH, Pinkert CA, Sharma A, Swanson ME;

PI White SP;

PS Claim 15; : 117pp; English.

The sequences given in AAR44521-28 represent mutant versions of the adult human beta globin sequence. These sequences were not given in the specification but were generated using the known beta globin sequence. These sequences were used in the production of constructs which were used to produce the transgenic pigs of the invention. These constructs contain the pig beta globin promoter sequence operably linked to the human alpha or beta globin genes. Pigs containing these constructs express human haemoglobin (Hb) in their erythrocytes and are healthy, suffering no deleterious side effects as a result of heterologous Hb production. They can be used as an efficient and economical source of human Hb that can be used for transfusion and other medical applications. Also, a human/pig hybrid Hb can be produced which exhibits a p50 that is higher than that of native human or pig Hb.

XX Sequence 146 AA:

Query Match 100.0%; Score 10; DB 15; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10

Db 32 lvvypwtgrf 41

RESULT 97

AA44524

AA44524 standard; Protein; 146 AA.

AC AA44524;

DE 23-JUN-1994 (first entry)

DE Adult human beta-globin A115L.

KW Adult; pig; beta; globin; gene; regulatory region; promoter;

KW transgenic pig; human; alpha; haemoglobin; Hb; erythrocyte;

OS Homo sapiens.

Key Location/Qualifiers

FT Misc-difference 115

/label= A115L

PN WO9325071-A.

PD 23-DEC-1993.

PF 11-JUN-1993; 93WO-US05629.

PR 12-JUN-1992; 92US-0897648.

PR 08-DEC-1992; 92US-0897890.

PR 15-MAR-1993; 93US-0030897.

PA (DNXD-) DNX CORP.

PI Holtzman SH, Kellier H, Kumar R, Logan JS, O' Donnell JK;

PI Parsons CT, Pilder SH, Pinkert CA, Sharma A, Swanson ME;

PI White SP;

DR WPI; 1994-007075/01.

PS Claim 15; : 117pp; English.

CC The sequences given in AA44521-28 represent mutant versions of the

CC adult human beta globin sequence. These sequences were not given in the

CC specification but were generated using the known beta globin sequence.

CC These sequences were used in the production of constructs which were

CC used to produce the transgenic pigs of the invention. These constructs

CC contain the pig beta globin promoter sequence operably linked to the

CC human alpha or beta globin genes. Pigs containing these constructs

CC express human haemoglobin (Hb) in their erythrocytes and are healthy,

CC suffering no deleterious side effects as a result of heterologous Hb

CC production. They can be used as an efficient and economical source of

CC human Hb that can be used for transfusion and other medical

CC applications. Also, a human/pig hybrid Hb can be produced which

CC exhibits a P50 that is higher than that of native human or pig Hb.

CC Sequence 146 AA;

SO

Query Match 100.0%; Score 10; DB 15; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00019;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTGRF 10

DB 32 lvvypwtgrf 41

RESULT 98

AA44525

AA44525 standard; Protein; 146 AA.

AC AA44525;

DE 23-JUN-1994 (first entry)

DE Adult human beta-globin G119H.

KW Adult; pig; beta; globin; gene; regulatory region; promoter;

KW transgenic pig; human; alpha; haemoglobin; Hb; erythrocyte;

KW transfusion; human/pig; hybrid Hb.

OS Homo sapiens.

Key Location/Qualifiers

FT Misc-difference 119

/label= G119H

PN WO9325071-A.

PD 23-DEC-1993.

PF 11-JUN-1993; 93WO-US05629.

PR 12-JUN-1992; 92US-0897648.

PR 08-DEC-1992; 92US-0897890.

PR 15-MAR-1993; 93US-0030897.

PA (DNXD-) DNX CORP.

PI Holtzman SH, Kellier H, Kumar R, Logan JS, O' Donnell JK;

PI Parsons CT, Pilder SH, Pinkert CA, Sharma A, Swanson ME;

PI White SP;

DR WPI; 1994-007075/01.

PS Claim 15; : 117pp; English.

CC The sequences given in AA44521-28 represent mutant versions of the

CC adult human beta globin sequence. These sequences were not given in the

CC specification but were generated using the known beta globin sequence.

CC These sequences were used in the production of constructs which were

CC used to produce the transgenic pigs of the invention. These constructs

CC contain the pig beta globin promoter sequence operably linked to the

CC human alpha or beta globin genes. Pigs containing these constructs

CC express human haemoglobin (Hb) in their erythrocytes and are healthy,

CC suffering no deleterious side effects as a result of heterologous Hb

CC production. They can be used as an efficient and economical source of

CC human Hb that can be used for transfusion and other medical

CC applications. Also, a human/pig hybrid Hb can be produced which

CC exhibits a P50 that is higher than that of native human or pig Hb.

CC Sequence 146 AA;

SO

Query Match 100.0%; Score 10; DB 15; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00019;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTGRF 10

DB 32 lvvypwtgrf 41

RESULT 99

AA44526

AA44526 standard; Protein; 146 AA.

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AC AAR44526;
XX
XX 23-JUN-1994 (first entry)
XX
XX Adult human beta-globin P128M(sic).
DE
XX Adult; pig; beta; globin; gene; regulatory region; promoter;
KW transgenic pig; human; alpha; haemoglobin; Hb; erythrocyte;
KW transfusion; human/pig; hybrid Hb.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 128
FT /label= P128M(sic)
FT
XX
XX W09325071-A.
XX
XX 23-DEC-1993.
XX
XX 11-JUN-1993; 93WO-US05629.
XX
XX 12-JUN-1992; 92US-0897648.
XX 08-DEC-1992; 92US-0987890.
XX 15-MAR-1993; 93US-0030897.
XX
XX (DNXD-) DNK CORP.
XX
XX Holtzman SH, Keller H, Kumar R, Logan JS, O' Donnell JK;
PI Parsons CT, Pilder SH, Pinkert CA, Sharma A, Swanson ME;
PI White SP;
XX
XX WPI: 1994-007075/01.
XX
XX Transgenic pigs which produce human haemoglobin - contg. DNA encoding
XX human alpha globin and huma beta globin linked to promoters
XX
XX Claim 15; : 117pp; English.
XX
XX The sequences given in AAR44521-28 represent mutant versions of the
XX adult human beta globin sequence. These sequences were not given in the
XX specification but were generated using the known beta globin sequence.
XX These sequences were used in the production of constructs which were
XX used to produce the transgenic pigs of the invention. These constructs
XX contain the pig beta globin promoter sequence operably linked to the
XX human alpha or beta globin genes. Pigs containing these constructs
XX express human haemoglobin (Hb) in their erythrocytes and are healthy,
XX suffering no deleterious side effects as a result of heterologous Hb
XX production. They can be used as an efficient and economical source of
XX human Hb that can be used for transfusion and other medical
XX applications. Also, a human/pig hybrid Hb can be produced which
XX exhibits a P50 that is higher than that of native human or pig Hb.
XX
XX Sequence 146 AA;
XX
XX Query Match 100.0%; Score 10; DB 15; Length 146;
XX Best Local Similarity 100.0%; Pred. No. 0.00019;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LVVYPWTGRF 10
DB 32 LVVYPWTGRF 41

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RESULT 100
AAR44527
ID AAR44527 standard; Protein: 146 AA.
XX
XX AAR44527;
XX
XX 23-JUN-1994 (first entry)
XX

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```

DE Adult human beta-globin Q131E.
XX
XX Adult; pig; beta; globin; gene; regulatory region; promoter;
KW transgenic pig; human; alpha; haemoglobin; Hb; erythrocyte;
KW transfusion; human/pig; hybrid Hb.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 131
FT /label= Q131E
FT
XX
XX W09325071-A.
XX
XX 23-DEC-1993.
XX
XX 11-JUN-1993; 93WO-US05629.
XX
XX 12-JUN-1992; 92US-0897648.
XX 08-DEC-1992; 92US-0987890.
XX 15-MAR-1993; 93US-0030897.
XX
XX (DNXD-) DNK CORP.
XX
XX Holtzman SH, Keller H, Kumar R, Logan JS, O' Donnell JK;
PI Parsons CT, Pilder SH, Pinkert CA, Sharma A, Swanson ME;
PI White SP;
XX
XX WPI: 1994-007075/01.
XX
XX Transgenic pigs which produce human haemoglobin - contg. DNA encoding
XX human alpha globin and huma beta globin linked to promoters
XX
XX Claim 15; : 117pp; English.
XX
XX The sequences given in AAR44521-28 represent mutant versions of the
XX adult human beta globin sequence. These sequences were not given in the
XX specification but were generated using the known beta globin sequence.
XX These sequences were used in the production of constructs which were
XX used to produce the transgenic pigs of the invention. These constructs
XX contain the pig beta globin promoter sequence operably linked to the
XX human alpha or beta globin genes. Pigs containing these constructs
XX express human haemoglobin (Hb) in their erythrocytes and are healthy,
XX suffering no deleterious side effects as a result of heterologous Hb
XX production. They can be used as an efficient and economical source of
XX human Hb that can be used for transfusion and other medical
XX applications. Also, a human/pig hybrid Hb can be produced which
XX exhibits a P50 that is higher than that of native human or pig Hb.
XX
XX Sequence 146 AA;
XX
XX Query Match 100.0%; Score 10; DB 15; Length 146;
XX Best Local Similarity 100.0%; Pred. No. 0.00019;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LVVYPWTGRF 10
DB 32 LVVYPWTGRF 41

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Page 45

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Gencore version 4.5
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OM protein - protein search, using sw model

Run on: July 1, 2002, 12:06:27 ; Search time 13.04 Seconds
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Title: US-09-147-490-1

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Searched: 231628 seqs, 24425594 residues

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Minimum DB seq length: 0

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Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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5	100.0	100.0	10	3	US-09-005-546-4
6	100.0	100.0	10	3	US-09-005-546-26
7	100.0	100.0	55	4	US-09-352-078-9
8	100.0	100.0	74	2	US-08-105-989-21
9	100.0	100.0	74	2	US-08-105-989-25
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12	100.0	100.0	143	4	US-09-230-603-22
13	100.0	100.0	144	4	US-09-230-603-21
14	100.0	100.0	146	1	US-07-923-692C-10
15	100.0	100.0	146	1	US-08-170-095B-2
16	100.0	100.0	146	1	US-08-184-337-10
17	100.0	100.0	146	1	US-08-240-712-19
18	100.0	100.0	146	1	US-08-240-712-20
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21	100.0	100.0	146	1	US-08-240-712-23
22	100.0	100.0	146	1	US-08-240-712-24
23	100.0	100.0	146	1	US-08-240-712-28
24	100.0	100.0	146	1	US-08-336-866-2
25	100.0	100.0	146	1	US-08-443-890-19
26	100.0	100.0	146	1	US-08-443-890-20
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28	100.0	146	1	US-08-443-890-22	Sequence 22, Appl
29	100.0	146	1	US-08-443-890-23	Sequence 23, Appl
30	100.0	146	1	US-08-443-890-24	Sequence 24, Appl
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39	100.0	146	2	US-08-482-920-10	Sequence 10, Appl
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46	100.0	146	3	US-08-381-175A-8	Sequence 8, Appl
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63	100.0	146	4	US-08-483-502-10	Sequence 10, Appl
64	100.0	146	4	US-09-352-078-1	Sequence 1, Appl
65	100.0	146	4	US-08-983-564A-33	Sequence 33, Appl
66	100.0	146	5	PCT-US92-09752-19	Sequence 19, Appl
67	100.0	146	5	PCT-US92-09752-20	Sequence 20, Appl
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71	100.0	146	5	PCT-US92-09752-24	Sequence 24, Appl
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87	90.0	146	3	US-09-005-546-27	Sequence 27, Appl
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91	80.0	8	2	US-08-535-882A-27	Sequence 27, Appl
92	80.0	8	3	US-09-005-546-6	Sequence 6, Appl
93	80.0	8	3	US-09-005-546-27	Sequence 27, Appl
94	70.0	7	2	US-08-627-173-10	Sequence 10, Appl
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98	70.0	7	2	US-08-535-882A-11	Sequence 11, Appl
99	70.0	7	2	US-08-981-384-1	Sequence 1, Appl
100	70.0	7	3	US-08-981-384-1	Sequence 1, Appl

ALIGNMENTS

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RESULT 1
US-08-627-173-4
; Sequence 4, Application US/08627173
; Patent No. 5861483
; GENERAL INFORMATION:
; APPLICANT: TSYRLOVA, IRENA
; APPLICANT: WOLPE, STEPHEN D.
; TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHAYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,173
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/535,882
; FILING DATE: 28-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 1331-177
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-627-173-4

Query Match          100.0%; Score 10; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 LVVYPWTORE 10

RESULT 2
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; Sequence 26, Application US/08627173
; Patent No. 5861483
; GENERAL INFORMATION:
; APPLICANT: TSYRLOVA, IRENA
; APPLICANT: WOLPE, STEPHEN D.
; TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHAYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
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; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,173
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/535,882
; FILING DATE: 28-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 1331-177
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-627-173-26
```

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Query Match          100.0%; Score 10; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTORE 10
   |||||
DB 1 LVVYPWTORE 10
```

```
RESULT 3
US-08-535-882A-4
; Sequence 4, Application US/08535882A
; Patent No. 5939391
; GENERAL INFORMATION:
; APPLICANT: TSYRLOVA, IRENA
; APPLICANT: WOLPE, STEPHEN D.
; TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHAYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,882A
; FILING DATE: 28-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 1331-177
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-535-882A-4

Query Match 100.0%; Score 10; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORF 10
|||||
DB 1 LVVYPWTORF 10

RESULT 4
US-08-535-882A-26
Sequence 26, Application US/08535882A
Patent No. 5939391
GENERAL INFORMATION:
APPLICANT: TSYRLOVA, IRENA
APPLICANT: WOLPE, STEPHEN D.
TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,882A
FILING DATE: 28-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1331-177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-535-882A-26

Query Match 100.0%; Score 10; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORF 10
|||||
DB 1 LVVYPWTORF 10

RESULT 5
US-09-005-546-4
Sequence 4, Application US/09005546
Patent No. 6090782
GENERAL INFORMATION:
APPLICANT: TSYRLOVA, IRENA
APPLICANT: WOLPE, STEPHEN D.
TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,546
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/535,882
FILING DATE: 28-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1331-177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-005-546-4

Query Match 100.0%; Score 10; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORF 10
|||||
DB 1 LVVYPWTORF 10

RESULT 6
US-09-005-546-26
Sequence 26, Application US/09005546
Patent No. 6090782
GENERAL INFORMATION:
APPLICANT: TSYRLOVA, IRENA
APPLICANT: WOLPE, STEPHEN D.
TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,546
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/535,882
FILING DATE: 28-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1331-177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-005-546-26

Query Match 100.0%; Score 10; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPTQRF 10
|||
Db 1 LVVYPTQRF 10

RESULT 7
US-09-352-078-9
Sequence 9, Application US/09352078
Patent No. 6337314
GENERAL INFORMATION:
APPLICANT: Theragem, Inc.
APPLICANT: Hoffman, Brian F.
APPLICANT: Dubnick, Bernard
TITLE OF INVENTION: USE OF MAMMALIAN-DERIVED PEPTIDES FOR
FILE REFERENCE: 1944/10999051
CURRENT APPLICATION NUMBER: US/09/352,078
CURRENT FILING DATE: 1999-07-14
EARLIER APPLICATION NUMBER: PCT/US98/16746
EARLIER FILING DATE: 1998-08-10
EARLIER APPLICATION NUMBER: 60/061,454
EARLIER FILING DATE: 1997-10-08
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 55
TYPE: PRT
ORGANISM: Homo sapiens
US-09-352-078-9

Query Match 100.0%; Score 10; DB 4; Length 55;
Best Local Similarity 100.0%; Pred. No. 8e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPTQRF 10
|||
Db 32 LVVYPTQRF 41

RESULT 8

US-08-105-989-21
Sequence 21, Application US/08105989
Patent No. 5922854
GENERAL INFORMATION:
APPLICANT: Kumar, Ramesh
APPLICANT: Sharma, Ajay
APPLICANT: Paulhac, Clara
APPLICANT: Khoury-Christianson, Anastasia P.
APPLICANT: Midha, Sunita
TITLE OF INVENTION: Production of Human Hemoglobin in
Transgenic Pigs.
TITLE OF INVENTION: Transgenic Pigs.
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/105,989
FILING DATE: 11-AUG-1993
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6794-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-105-989-21

Query Match 100.0%; Score 10; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPTQRF 10
|||
Db 2 LVVYPTQRF 11

RESULT 9
US-08-105-989-25
Sequence 25, Application US/08105989
Patent No. 5922854
GENERAL INFORMATION:
APPLICANT: Kumar, Ramesh
APPLICANT: Sharma, Ajay
APPLICANT: Paulhac, Clara
APPLICANT: Khoury-Christianson, Anastasia P.
APPLICANT: Midha, Sunita
TITLE OF INVENTION: Production of Human Hemoglobin in
Transgenic Pigs.
TITLE OF INVENTION: Transgenic Pigs.
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.

ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/105,989
FILING DATE: 11-AUG-1993
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6794-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-105-989-25

Query Match 100.0%; Score 10; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
Db 2 LVVYPWTQRF 11

RESULT 10
US-09-138-922-21
Sequence 21, Application US/09138922
Patent No. 6147202
GENERAL INFORMATION:
APPLICANT: Kumar, Ramesh
APPLICANT: Sharma, Ajay
APPLICANT: Paulhiac, Clara
APPLICANT: Khoury-Christianson, Anastasia P.
APPLICANT: Midha, Sunita
TITLE OF INVENTION: Production of Human Hemoglobin in
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,922
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/105,989
FILING DATE: 11-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6794-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-138-922-25

TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-138-922-21

Query Match 100.0%; Score 10; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
Db 2 LVVYPWTQRF 11

RESULT 11
US-09-138-922-25
Sequence 25, Application US/09138922
Patent No. 6147202
GENERAL INFORMATION:
APPLICANT: Kumar, Ramesh
APPLICANT: Sharma, Ajay
APPLICANT: Paulhiac, Clara
APPLICANT: Khoury-Christianson, Anastasia P.
APPLICANT: Midha, Sunita
TITLE OF INVENTION: Production of Human Hemoglobin in
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,922
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/105,989
FILING DATE: 11-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6794-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-138-922-25

Query Match 100.0%; Score 10; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
|1111111111
DB 2 LVVYPWTORE 11

RESULT 12
US-09-230-603-22
; Sequence 22, Application US/09230603
; Patent No. 6171826
; GENERAL INFORMATION:
; APPLICANT: LEVINE, JOSEPH D
; APPLICANT: APOSTOL, IZYDOR A
; TITLE OF INVENTION: METHODS OF CONTROLLING BETA DIMER FORMATION IN
; FILE REFERENCE: BXTB3060
; CURRENT FILING DATE: 1999-05-14
; EARLIER FILING DATE: 1997-08-01
; EARLIER APPLICATION NUMBER: 60/023,211
; EARLIER FILING DATE: 1996-08-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: NON_TER
; LOCATION: (1)
; OTHER INFORMATION: the N-terminal methionine residue incorporated
; OTHER INFORMATION: during the translation initiation step is excised
; OTHER INFORMATION: during translation and is not present in the
; OTHER INFORMATION: mature polypeptide chain
US-09-230-603-22

Query Match 100.0%; Score 10; DB 4; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
|1111111111
DB 33 LVVYPWTORE 42

RESULT 13
US-09-230-603-21
; Sequence 21, Application US/09230603
; Patent No. 6171826
; GENERAL INFORMATION:
; APPLICANT: LEVINE, JOSEPH D
; APPLICANT: APOSTOL, IZYDOR A
; TITLE OF INVENTION: METHODS OF CONTROLLING BETA DIMER FORMATION IN
; FILE REFERENCE: BXTB3060
; CURRENT FILING DATE: 1999-05-14
; EARLIER FILING DATE: 1997-08-01
; EARLIER APPLICATION NUMBER: 60/023,211
; EARLIER FILING DATE: 1996-08-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: NON_TER
; LOCATION: (1)
; OTHER INFORMATION: the N-terminal methionine residue incorporated

; OTHER INFORMATION: during the translation initiation step is excised
; OTHER INFORMATION: during the translation and is not present in the
; OTHER INFORMATION: mature polypeptide chain
US-09-230-603-21

Query Match 100.0%; Score 10; DB 4; Length 144;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
|1111111111
DB 33 LVVYPWTORE 42

RESULT 14
US-07-923-692C-10
; Sequence 10, Application US/07923692C
; Patent No. 5316931
; GENERAL INFORMATION:
; APPLICANT: Dawson, Jon
; APPLICANT: Grantam, George O.
; APPLICANT: Turpen, Thomas H.
; APPLICANT: Turpen, Ann Myers
; APPLICANT: Garger, Stephen J.
; APPLICANT: Grill, Laurence K.
; TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESS: Limbach & Limbach
; STREET: 2001 Ferry Building
; CITY: San Francisco
; STATE: CAL
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/923,692C
; FILING DATE: 31-JUL-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 600,244
; FILING DATE: 22-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 641,617
; FILING DATE: 16-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 310,881
; FILING DATE: 17-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 160,766
; FILING DATE: 26-FEB-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 160,771
; FILING DATE: 26-FEB-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 347,637
; FILING DATE: 05-MAY-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 363,138
; FILING DATE: 08-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 219,279
; FILING DATE: 15-JUL-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: BIOG-20121
; REFERENCE/DOCKET NUMBER: USA

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-4150
TELEFAX: 415-433-8716
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-923-692C-10

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPTQRF 10
|||||
DB 32 LVVYPTQRF 41

RESULT 15
US-08-170-095B-2
Sequence 2, Application US/08170095B
Patent No. 5563254
GENERAL INFORMATION:
APPLICANT: Hoffman, Stephen J.
APPLICANT: Nagai, Kiyoshi
TITLE OF INVENTION: Blood Substitutes
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Somatogen, Inc.
STREET: 2545 Central Avenue
CITY: Boulder
STATE: Colorado
ZIP: 80301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.0.1
SOFTWARE: Microsoft Word 5.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/170,095B
FILING DATE: December 20, 1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: No. 5563254ak, Henry P.
REGISTRATION NUMBER: 33200
REFERENCE/DOCKET NUMBER: Hoffman 2A/CONT2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-541-3322
TELEFAX: 303-444-3013
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 146
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown to applicant
MOLECULE TYPE: protein
HYPOTHETICAL: no
US-08-170-095B-2

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPTQRF 10
|||||
DB 32 LVVYPTQRF 41

RESULT 16

US-08-184-237-10
Sequence 10; Application US/08184237
Patent No. 5589367
GENERAL INFORMATION:
APPLICANT: Dawson, Jon
APPLICANT: Dawson, William O.
APPLICANT: Grantham, George L.
APPLICANT: Turpen, Thomas H.
APPLICANT: Turpen, Ann Myers
APPLICANT: Garger, Stephen J.
APPLICANT: Grill, Laurence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Limbach & Limbach
STREET: 2001 Ferry Building
CITY: San Francisco
STATE: CAL
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,237
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 923,692
FILING DATE: 31-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,771
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 347,637
FILING DATE: 05-MAY-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 219,279
FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: BIOG-20121 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-4150
TELEFAX: 415-433-8716
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-184-237-10

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPMWTFORF 10
|||||
Db 32 LVVYPMWTFORF 41

RESULT 17
US-08-240-712-19
Sequence 19, Application US/08240712
Patent No. 5599907
GENERAL INFORMATION:
APPLICANT: ANDERSON, DAVID C.
APPLICANT: MATHEWS, ANTONY JAMES
APPLICANT: STETLER, GARY L.
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
TITLE OF INVENTION: HEMOGLOBINS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240.712
FILING DATE: 09-MAY-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09752
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IYER P
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: ANDERSON-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-240-712-19

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPMWTFORF 10
|||||
Db 32 LVVYPMWTFORF 41

RESULT 18
US-08-240-712-20
Sequence 20, Application US/08240712
Patent No. 5599907
GENERAL INFORMATION:
APPLICANT: ANDERSON, DAVID C.
APPLICANT: MATHEWS, ANTONY JAMES
APPLICANT: STETLER, GARY L.
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC

TITLE OF INVENTION: HEMOGLOBINS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240.712
FILING DATE: 09-MAY-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09752
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IYER P
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: ANDERSON-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-240-712-20

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPMWTFORF 10
|||||
Db 32 LVVYPMWTFORF 41

RESULT 19
US-08-240-712-21
Sequence 21, Application US/08240712
Patent No. 5599907
GENERAL INFORMATION:
APPLICANT: ANDERSON, DAVID C.
APPLICANT: MATHEWS, ANTONY JAMES
APPLICANT: STETLER, GARY L.
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
TITLE OF INVENTION: HEMOGLOBINS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240.712

FILED DATE: 09-MAY-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09752
FILED DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: ANDERSON-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-240-712-21

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFORF 10
|||||
DB 32 LVVYPWTFORF 41

RESULT 20
US-08-240-712-22
Sequence 22, Application US/08240712
Patent No. 5599907
GENERAL INFORMATION:
APPLICANT: ANDERSON, DAVID C.
APPLICANT: MATHEWS, ANTONY JAMES
APPLICANT: STELLER, GARY L.
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,712
FILED DATE: 09-MAY-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09752
FILED DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: ANDERSON-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-240-712-22

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFORF 10
|||||
DB 32 LVVYPWTFORF 41

RESULT 21
US-08-240-712-23
Sequence 23, Application US/08240712
Patent No. 5599907
GENERAL INFORMATION:
APPLICANT: ANDERSON, DAVID C.
APPLICANT: MATHEWS, ANTONY JAMES
APPLICANT: STELLER, GARY L.
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,712
FILED DATE: 09-MAY-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09752
FILED DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: ANDERSON-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-240-712-23

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFORF 10
|||||
DB 32 LVVYPWTFORF 41

RESULT 22
US-08-240-712-24
Sequence 24, Application US/08240712
Patent No. 5599907
GENERAL INFORMATION:
APPLICANT: ANDERSON, DAVID C.
APPLICANT: MATHEWS, ANTONY JAMES
APPLICANT: STETLER, GARY L.
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240.712
FILING DATE: 09-MAY-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09752
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IYER P
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: ANDERSON-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-240-712-24

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVYPWTFORF 10
DB 32 LVVYPWTFORF 41

RESULT 23
US-08-240-712-28
Sequence 28, Application US/08240712
Patent No. 5599907
GENERAL INFORMATION:
APPLICANT: ANDERSON, DAVID C.
APPLICANT: MATHEWS, ANTONY JAMES
APPLICANT: STETLER, GARY L.
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.

COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240.712
FILING DATE: 09-MAY-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09752
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IYER P
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: ANDERSON-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-240-712-28

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVYPWTFORF 10
DB 32 LVVYPWTFORF 41

RESULT 24
US-08-396-866-2
Sequence 2, Application US/08396866
Patent No. 5661124
GENERAL INFORMATION:
APPLICANT: Hoffman, Stephen J.
APPLICANT: Nagai, Kiyoshi
TITLE OF INVENTION: Blood Substitutes
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Somatogen, Inc.
STREET: 5797 Central Avenue
CITY: Boulder
STATE: Colorado
ZIP: 80301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.0.1
SOFTWARE: Microsoft word 5.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/396.866
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/062.780
FILING DATE: May 17, 1993
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5661124ak, Henry P.
REGISTRATION NUMBER: 35200
REFERENCE/DOCKET NUMBER: Hoffman
REFERENCE/DOCKET NUMBER: 2A/CONT1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-541-3322
TELEFAX: 303-444-3013
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 146
TYPE: amino acid
TOPOLOGY: unknown to applicant
MOLECULE TYPE: protein
HYPOTHETICAL: no
US-08-396-866-2

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTFQRF 10
Db 32 LVVYPWTFQRF 41

RESULT 25
US-08-443-890-19
Sequence 19, Application US/08443890
Patent No. 5739011
GENERAL INFORMATION:
APPLICANT: ANDERSON, DAVID C.
APPLICANT: MATHEWS, ANTONY JAMES
APPLICANT: STETTLER, GARY L.
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Broadway and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,890
FILING DATE: 31-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/240,712
FILING DATE: 09-MAY-1994
APPLICATION NUMBER: PCT/US92/09752
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: ANDERSON-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-443-890-19
Query Match 100.0%; Score 10; DB 1; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTFQRF 10
Db 32 LVVYPWTFQRF 41

RESULT 26
US-08-443-890-20
Sequence 20, Application US/08443890
Patent No. 5739011
GENERAL INFORMATION:
APPLICANT: ANDERSON, DAVID C.
APPLICANT: MATHEWS, ANTONY JAMES
APPLICANT: STETTLER, GARY L.
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Broadway and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,890
FILING DATE: 31-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/240,712
FILING DATE: 09-MAY-1994
APPLICATION NUMBER: PCT/US92/09752
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: ANDERSON-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-443-890-20
Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTFQRF 10
Db 32 LVVYPWTFQRF 41

RESULT 27
US-08-443-890-21
Sequence 21, Application US/08443890
Patent No. 5739011
GENERAL INFORMATION:
APPLICANT: ANDERSON, DAVID C.

APPLICANT: MATTHEWS, ANTONY JAMES
APPLICANT: SETTLER, GARY L.
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
TITLE OF INVENTION: HEMOGLOBINS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,890
FILING DATE: 31-MAY-1995
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/240,712
FILING DATE: 09-MAY-1994
APPLICATION NUMBER: PCT/US92/09752
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: ANDERSON-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-443-890-21

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPTQRF 10
DB 32 LVVYPTQRF 41

RESULT 28
US-08-443-890-22
Sequence 22, Application US/08443890
Patent No. 5739011
GENERAL INFORMATION:
APPLICANT: ANDERSON, DAVID C.
APPLICANT: MATTHEWS, ANTONY JAMES
APPLICANT: SETTLER, GARY L.
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
TITLE OF INVENTION: HEMOGLOBINS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,890
FILING DATE: 31-MAY-1995
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/240,712
FILING DATE: 09-MAY-1994
APPLICATION NUMBER: PCT/US92/09752
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: ANDERSON-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-443-890-22

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPTQRF 10
DB 32 LVVYPTQRF 41

RESULT 29
US-08-443-890-23
Sequence 23, Application US/08443890
Patent No. 5739011
GENERAL INFORMATION:
APPLICANT: ANDERSON, DAVID C.
APPLICANT: MATTHEWS, ANTONY JAMES
APPLICANT: SETTLER, GARY L.
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
TITLE OF INVENTION: HEMOGLOBINS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,890
FILING DATE: 31-MAY-1995
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/240,712
FILING DATE: 09-MAY-1994
APPLICATION NUMBER: PCT/US92/09752
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P

REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: ANDERSON-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-443-890-23

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFORF 10
|||||
Db 32 LVVYPWTFORF 41

RESULT 30
US-08-443-890-24
Sequence 24, Application US/08443890
Patent No. 5739011
GENERAL INFORMATION:
APPLICANT: ANDERSON, DAVID C.
APPLICANT: MATHEWS, ANTONY JAMES
APPLICANT: STETLER, GARY L.
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,890
FILING DATE: 31-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/240,712
FILING DATE: 09-MAY-1994
APPLICATION NUMBER: PCT/US92/09752
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: ANDERSON-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-443-890-24

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFORF 10
|||||
Db 32 LVVYPWTFORF 41

RESULT 31
US-08-443-890-28
Sequence 28, Application US/08443890
Patent No. 5739011
GENERAL INFORMATION:
APPLICANT: ANDERSON, DAVID C.
APPLICANT: MATHEWS, ANTONY JAMES
APPLICANT: STETLER, GARY L.
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,890
FILING DATE: 31-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/240,712
FILING DATE: 09-MAY-1994
APPLICATION NUMBER: PCT/US92/09752
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: ANDERSON-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-443-890-28

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFORF 10
|||||
Db 32 LVVYPWTFORF 41

RESULT 32
US-08-484-686B-66
Sequence 66, Application US/08484686B

Patent No. 5827693
GENERAL INFORMATION:
APPLICANT: De Angelo, Joseph
APPLICANT: Motwani, Nalini
APPLICANT: Bajwa, Waheen
TITLE OF INVENTION: Expression of Recombinant Hemoglobin and
Hemoglobin Variants in Yeast
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennle & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,686B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/368,407
FILING DATE: 29-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/876,290
FILING DATE: 29-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/684,611
FILING DATE: 12-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Flintoft, Gerald J.
REGISTRATION NUMBER: 20,823
REFERENCE/DOCKET NUMBER: 6666-043-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-484-686B-66

Query Match 100.0%; Score 10; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LVVYPWTQRF 10
DB 32 LVVYPWTQRF 41

RESULT 33
US-08-484-686B-67
Sequence 67, Application US/08484686B
Patent No. 5827693
GENERAL INFORMATION:
APPLICANT: De Angelo, Joseph
APPLICANT: Motwani, Nalini
APPLICANT: Bajwa, Waheen
TITLE OF INVENTION: Expression of Recombinant Hemoglobin and
Hemoglobin Variants in Yeast
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennle & Edmonds LLP

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,686B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/368,407
FILING DATE: 29-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/876,290
FILING DATE: 29-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/684,611
FILING DATE: 12-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Flintoft, Gerald J.
REGISTRATION NUMBER: 20,823
REFERENCE/DOCKET NUMBER: 6666-043-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-484-686B-67

Query Match 100.0%; Score 10; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LVVYPWTQRF 10
DB 32 LVVYPWTQRF 41

RESULT 34
US-08-484-686B-68
Sequence 68, Application US/08484686B
Patent No. 5827693
GENERAL INFORMATION:
APPLICANT: De Angelo, Joseph
APPLICANT: Motwani, Nalini
APPLICANT: Bajwa, Waheen
TITLE OF INVENTION: Expression of Recombinant Hemoglobin and
Hemoglobin Variants in Yeast
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennle & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,686B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/368,407
FILING DATE: 29-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/876,290
FILING DATE: 29-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/684,611
FILING DATE: 12-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Flintoft, Gerald J.
REGISTRATION NUMBER: 20,823
REFERENCE/DOCKET NUMBER: 6666-043-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-484-686B-68

Query Match 100.0%; Score 10; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFORF 10
|||
Db 32 LVVYPWTFORF 41

RESULT 35
US-08-484-686B-70
Sequence 70, Application US/08484686B
Patent No. 5827693
GENERAL INFORMATION:
APPLICANT: De Angelo, Joseph
APPLICANT: Motwani, Nalin
APPLICANT: Bajwa, Wajeeh
TITLE OF INVENTION: Expression of Recombinant Hemoglobin and
TITLE OF INVENTION: Hemoglobin Variants in Yeast
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,686B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/368,407
FILING DATE: 29-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/876,290
FILING DATE: 29-APR-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/684,611
FILING DATE: 12-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Flintoft, Gerald J.
REGISTRATION NUMBER: 20,823
REFERENCE/DOCKET NUMBER: 6666-043-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-484-686B-70

Query Match 100.0%; Score 10; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFORF 10
|||
Db 32 LVVYPWTFORF 41

RESULT 36
US-08-432-071B-4
Sequence 4, Application US/08432071B
Patent No. 5843888
GENERAL INFORMATION:
APPLICANT: Ho, Chien
APPLICANT: Kim, Hyun-Mon
APPLICANT: Shen, Tong-Jian
TITLE OF INVENTION: Low Oxygen
TITLE OF INVENTION: Affinity Mutant Hemoglobin
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carnegie Mellon University
STREET: 4400 Forbes Avenue
CITY: Pittsburgh
STATE: Pennsylvania
COUNTRY: USA
ZIP: 15213
COMPUTER READABLE FORM:
MEDIUM TYPE: 5-1/4 low density diskette
COMPUTER: IBM PC or compatibles
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,071B
FILING DATE: 01-MAY-95
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: No. 5843888 applicable
FILING DATE: No. 5843888 applicable
ATTORNEY/AGENT INFORMATION:
NAME: Mary-Elizabeth Buckles
REGISTRATION NUMBER: 31,907
REFERENCE/DOCKET NUMBER: CM095-040
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/414-9200
TELEFAX: 202/414-9299
TELEX: 64711
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
DESCRIPTION: human -globin amino acid
US-08-432-0718-4

Query Match 100.0%; Score 10; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
|||||
DB 32 LVVYPWTQRF 41

RESULT 37
US-08-627-173-18
Sequence 18 Application US/08627173
Patent No. 5861483
GENERAL INFORMATION:
APPLICANT: TSYRLOVA, IRENA
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
NUMBER OF SEQUENCES: 27
TITLE OF INVENTION: USES THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,173
FILING DATE: 03-APR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/535,882
FILING DATE: 28-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1331-177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ. ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-627-173-18

Query Match 100.0%; Score 10; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
|||||
DB 32 LVVYPWTQRF 41

RESULT 38
US-08-627-173-22
Sequence 22 Application US/08627173

Patent No. 5861483
GENERAL INFORMATION:
APPLICANT: TSYRLOVA, IRENA
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
NUMBER OF SEQUENCES: 27
TITLE OF INVENTION: USES THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,173
FILING DATE: 03-APR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/535,882
FILING DATE: 28-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1331-177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ. ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-627-173-22

Query Match 100.0%; Score 10; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
|||||
DB 32 LVVYPWTQRF 41

RESULT 39
US-08-482-920-10
Sequence 10 Application US/08482920
Patent No. 5866785
GENERAL INFORMATION:
APPLICANT: Dawson, Jon
APPLICANT: Dawson, William O.
APPLICANT: Grantham, George L.
APPLICANT: Turpen, Thomas H.
APPLICANT: Turpen, Ann Myers
APPLICANT: Garger, Stephen J.
APPLICANT: Grill, Laurence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
ZIP: 10036
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,920
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 184,237
FILING DATE: 19-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,771
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 347,637
FILING DATE: 05-MAY-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 219,279
FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 8129-112
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-920-10

Query Match 100.0%; Score 10; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFQRF 10
Db 32 LVVYPWTFQRF 41

RESULT 40
US-08-535-882A-18
Sequence 18, Application US/08535882A
Patent No. 5939391
GENERAL INFORMATION:
APPLICANT: TSYRLOVA, IRENA
APPLICANT: WOLPE, STEPHEN D.
TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON

STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,882A
FILING DATE: 28-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1331-177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-535-882A-18

Query Match 100.0%; Score 10; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFQRF 10
Db 32 LVVYPWTFQRF 41

RESULT 41
US-08-535-882A-22
Sequence 22, Application US/08535882A
Patent No. 5939391
GENERAL INFORMATION:
APPLICANT: TSYRLOVA, IRENA
APPLICANT: WOLPE, STEPHEN D.
TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,882A
FILING DATE: 28-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1331-177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:

LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-535-882A-22

Query Match 100.0%; Score 10; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTFORF 10
|||||
DB 32 LVVYPWTFORF 41

RESULT 42
US-08-619-708A-6
Sequence 6, Application US/08619708A
Patent No. 5942488
GENERAL INFORMATION:
APPLICANT: Komiya, No. 5942488oru
APPLICANT: Nagai, Kiyoshi
TITLE OF INVENTION: Improvements In Or Relating To
TITLE OF INVENTION: Haemoglobin
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Somatogen, Inc.
STREET: 2545 Central Avenue, Suite FDI
CITY: Boulder
STATE: Colorado
ZIP: 80301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,708A
FILING DATE: 17 JUNE 1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB94/01996
FILING DATE: 13 SEPT. 1994
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Theresa A.
REGISTRATION NUMBER: 32,547
REFERENCE/DOCKET NUMBER: 280
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-541-3356
TELEFAX: 303-444-3013
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 146
TYPE: amino acid
TOPOLOGY: unknown to applicant
MOLECULE TYPE: protein
HYPOTHETICAL: no
US-08-619-708A-6

Query Match 100.0%; Score 10; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTFORF 10
|||||
DB 32 LVVYPWTFORF 41

RESULT 43
US-08-316-424A-4

Sequence 4, Application US/08316424A
Patent No. 6022848
GENERAL INFORMATION:
APPLICANT: KOZLOV, VLADIMIR
APPLICANT: TSYROVA, IRENA
TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,424A
FILING DATE: 30-SEP-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1331-122
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-316-424A-4

Query Match 100.0%; Score 10; DB 3; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTFORF 10
|||||
DB 32 LVVYPWTFORF 41

RESULT 44
US-08-316-424A-8
Sequence 8, Application US/08316424A
Patent No. 6022848
GENERAL INFORMATION:
APPLICANT: KOZLOV, VLADIMIR
APPLICANT: TSYROVA, IRENA
TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/316,424A
FILING DATE: 30-SEP-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1331-122
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-316-424A-8

Query Match 100.0%; Score 10; DB 3; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
|||1111111111
DB 32 LVVYPWTQRF 41

RESULT 45

US-08-381-175A-2
Sequence 2, Application US/08381175A
Patent No. 6022849

GENERAL INFORMATION:
APPLICANT: Olson, John S.
APPLICANT: Aitken, Jacqueline F.
APPLICANT: Mathews, Antony J.
APPLICANT: Nagai, Kiyoshi
TITLE OF INVENTION: Mutant Recombinant Hemoglobins Containing Heme Pocket Muta
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Somatogen, Inc.
STREET: 2545 Central Avenue, Suite FDI
CITY: Boulder
STATE: Colorado
ZIP: 80301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.0.1
SOFTWARE: Microsoft Word 5.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,175A
FILING DATE: 31-JAN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/158,483
FILING DATE: 29-NOV-1993
APPLICATION NUMBER: 07/443,950
FILING DATE: 12-DEC-1989
APPLICATION NUMBER: 07/194,338
FILING DATE: 16-MAY-1988
ATTORNEY/AGENT INFORMATION:
NAME: No. 6022849e111, Marianne F.
REGISTRATION NUMBER: 38751
REFERENCE/DOCKET NUMBER: 220
NAME: Brown, Theresa A.
REGISTRATION NUMBER: 32547
REFERENCE/DOCKET NUMBER: 220
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-541-3324
TELEFAX: 303-444-3013
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 146
TYPE: amino acid
TOPOLOGY: unknown to applicant
MOLECULE TYPE: protein
HYPOTHETICAL: no
US-08-381-175A-2

Query Match 100.0%; Score 10; DB 3; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
|||1111111111
DB 32 LVVYPWTQRF 41

RESULT 46

US-08-381-175A-8
Sequence 8, Application US/08381175A
Patent No. 6022849

GENERAL INFORMATION:
APPLICANT: Olson, John S.
APPLICANT: Aitken, Jacqueline F.
APPLICANT: Mathews, Antony J.
APPLICANT: Nagai, Kiyoshi
TITLE OF INVENTION: Mutant Recombinant Hemoglobins Containing Heme Pocket Muta
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Somatogen, Inc.
STREET: 2545 Central Avenue, Suite FDI
CITY: Boulder
STATE: Colorado
ZIP: 80301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.0.1
SOFTWARE: Microsoft Word 5.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,175A
FILING DATE: 31-JAN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/158,483
FILING DATE: 29-NOV-1993
APPLICATION NUMBER: 07/443,950
FILING DATE: 12-DEC-1989
APPLICATION NUMBER: 07/194,338
FILING DATE: 16-MAY-1988
ATTORNEY/AGENT INFORMATION:
NAME: No. 6022849e111, Marianne F.
REGISTRATION NUMBER: 38751
REFERENCE/DOCKET NUMBER: 220
NAME: Brown, Theresa A.
REGISTRATION NUMBER: 32547
REFERENCE/DOCKET NUMBER: 220
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-541-3324
TELEFAX: 303-444-3013
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 146
TYPE: amino acid
TOPOLOGY: unknown to applicant
MOLECULE TYPE:
DESCRIPTION: beta globin protein sequence as expressed in E. coli
HYPOTHETICAL: no
US-08-381-175A-8

Query Match 100.0%; Score 10; DB 3; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFORF 10
| | | | | | | | | |
Db 32 LVVYPWTFORF 41

RESULT 47

US-08-484-341-10
Sequence 10, Application US/08484341

GENERAL INFORMATION:

APPLICANT: Donson, Jon
Dawson, William O.
Grantam, George L.
Turpen, Thomas H.
Turpen, Ann Myers
Garger, Stephen J.
Grill, Laurence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Limbach & Limbach
STREET: 2001 Ferry Building
CITY: San Francisco
STATE: CAL
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,341
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/184,237
FILING DATE: <Unknown>
APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
APPLICATION NUMBER: US 160,771
FILING DATE: 26-FEB-1988
APPLICATION NUMBER: US 347,637
FILING DATE: 05-MAY-1989
APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1988
APPLICATION NUMBER: US 219,279
FILING DATE: 15-JUL-1988

ATTORNEY/AGENT INFORMATION:

NAME: Halluin, Albert P.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: BIOG-20121 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-4150
TELEFAX: 415-433-8716

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-08-484-341-10

Query Match 100.0%; Score 10; DB 3; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFORF 10
| | | | | | | | | |
Db 32 LVVYPWTFORF 41

RESULT 48

US-09-005-546-18
Sequence 18, Application US/09005546

GENERAL INFORMATION:

APPLICANT: TSYRLOVA, IRENA
APPLICANT: WOLPE, STEPHEN D.
TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,546
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/535,882
FILING DATE: 28-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1331-177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4000
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-005-546-18

Query Match 100.0%; Score 10; DB 3; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFORF 10
| | | | | | | | | |
Db 32 LVVYPWTFORF 41

RESULT 49

US-09-005-546-22
Sequence 22, Application US/09005546

GENERAL INFORMATION:

APPLICANT: TSYRLOVA, IRENA
APPLICANT: WOLPE, STEPHEN D.
TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
NUMBER OF SEQUENCES: 27

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: NIXON & VANDERHVE P.C.
;; STREET: 1100 NORTH GLEBE ROAD
;; CITY: ARLINGTON
;; STATE: VIRGINIA
;; COUNTRY: U.S.A.
;; ZIP: 22201-4714
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/005,546
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/535,882
;; FILING DATE: 28-SEP-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BYRNE, THOMAS E.
;; REGISTRATION NUMBER: 32,205
;; REFERENCE/DOCKET NUMBER: 1331-177
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 816-4000
;; TELEFAX: (703) 816-4100
;; INFORMATION FOR SEQ ID NO: 22:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 146 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;;
US-09-005-546-22

Query Match 100.0%; Score 10; DB 3; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
Db 32 LVVYPWTQRF 41

RESULT 50
US-09-230-603-2
; Sequence 2, Application US/09230603
; Patent No. 6171826
; GENERAL INFORMATION:
; APPLICANT: LEVINE, JOSEPH D
; APPLICANT: APOSTOL, IZDOR A
; TITLE OF INVENTION: METHODS OF CONTROLLING BETA DIMER FORMATION IN
; TITLE OF INVENTION: HEMOGLOBIN
; FILE REFERENCE: BXTB3060
; CURRENT APPLICATION NUMBER: US/09/230,603
; CURRENT FILING DATE: 1999-05-14
; EARLIER APPLICATION NUMBER: PCT/US97/13564
; EARLIER FILING DATE: 1997-08-01
; EARLIER APPLICATION NUMBER: 60/023,211
; EARLIER FILING DATE: 1996-08-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 146
; TYPE: PRT
; ORGANISM: HUMAN BETA GLOBIN
US-09-230-603-2

Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
Db 32 LVVYPWTQRF 41

RESULT 51
US-09-230-603-12
; Sequence 12, Application US/09230603
; Patent No. 6171826
; GENERAL INFORMATION:
; APPLICANT: LEVINE, JOSEPH D
; APPLICANT: APOSTOL, IZDOR A
; TITLE OF INVENTION: METHODS OF CONTROLLING BETA DIMER FORMATION IN
; TITLE OF INVENTION: HEMOGLOBIN
; FILE REFERENCE: BXTB3060
; CURRENT APPLICATION NUMBER: US/09/230,603
; CURRENT FILING DATE: 1999-05-14
; EARLIER APPLICATION NUMBER: PCT/US97/13564
; EARLIER FILING DATE: 1997-08-01
; EARLIER APPLICATION NUMBER: 60/023,211
; EARLIER FILING DATE: 1996-08-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-230-603-12

Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
Db 32 LVVYPWTQRF 41

RESULT 52
US-09-230-603-13
; Sequence 13, Application US/09230603
; Patent No. 6171826
; GENERAL INFORMATION:
; APPLICANT: LEVINE, JOSEPH D
; APPLICANT: APOSTOL, IZDOR A
; TITLE OF INVENTION: METHODS OF CONTROLLING BETA DIMER FORMATION IN
; TITLE OF INVENTION: HEMOGLOBIN
; FILE REFERENCE: BXTB3060
; CURRENT APPLICATION NUMBER: US/09/230,603
; CURRENT FILING DATE: 1999-05-14
; EARLIER APPLICATION NUMBER: PCT/US97/13564
; EARLIER FILING DATE: 1997-08-01
; EARLIER APPLICATION NUMBER: 60/023,211
; EARLIER FILING DATE: 1996-08-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-230-603-13

Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
Db 32 LVVYPWTQRF 41

RESULT 53
US-09-230-603-17
; Sequence 17, Application US/09230603
; Patent No. 6171826
; GENERAL INFORMATION:
; APPLICANT: LEVINE, JOSEPH D
; APPLICANT: APOSTOL, IZYDOR A
; TITLE OF INVENTION: METHODS OF CONTROLLING BETA DIMER FORMATION IN
; TITLE OF INVENTION: HEMOGLOBIN
; FILE REFERENCE: BXTB3060
; CURRENT APPLICATION NUMBER: US/09/230,603
; CURRENT FILING DATE: 1999-05-14
; EARLIER APPLICATION NUMBER: PCT/US97/13564
; EARLIER FILING DATE: 1997-08-01
; EARLIER APPLICATION NUMBER: 60/023,211
; EARLIER FILING DATE: 1996-08-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-230-603-17

Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTWTF 10
|||||
Db 32 LVVYPTWTF 41

RESULT 54
US-09-230-603-20
; Sequence 20, Application US/09230603
; Patent No. 6171826
; GENERAL INFORMATION:
; APPLICANT: LEVINE, JOSEPH D
; APPLICANT: APOSTOL, IZYDOR A
; TITLE OF INVENTION: METHODS OF CONTROLLING BETA DIMER FORMATION IN
; TITLE OF INVENTION: HEMOGLOBIN
; FILE REFERENCE: BXTB3060
; CURRENT APPLICATION NUMBER: US/09/230,603
; CURRENT FILING DATE: 1999-05-14
; EARLIER APPLICATION NUMBER: PCT/US97/13564
; EARLIER FILING DATE: 1997-08-01
; EARLIER APPLICATION NUMBER: 60/023,211
; EARLIER FILING DATE: 1996-08-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: NON_TER
; LOCATION: (1)
; OTHER INFORMATION: the N-terminal methionine residue incorporated
; OTHER INFORMATION: during the translation initiation step is excised
; OTHER INFORMATION: during translation and is not present in the
; OTHER INFORMATION: mature polypeptide chain
US-09-230-603-20

Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTWTF 10
|||||

Db 33 LVVYPTWTF 42

RESULT 55
US-08-463-160B-67
; Sequence 67, Application US/08463160B
; Patent No. 6172039
; GENERAL INFORMATION:
; APPLICANT: De Angelo, Joseph
; APPLICANT: Motwani, Nalini
; APPLICANT: Bajwa, Waheem
; TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HEMOGLOBIN
; TITLE OF INVENTION: AND HEMOGLOBIN VARIANTS IN YEAST
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,160B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/368,407
; FILING DATE: 29-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/876,290
; FILING DATE: 29-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/684,611
; FILING DATE: 12-APR-1991
; ATORCNEY/AGENT INFORMATION:
; NAME: Flintoft, Gerald J.
; REGISTRATION NUMBER: 20,823
; REFERENCE/DOCKET NUMBER: 6666-044-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELE: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-463-160B-67

Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTWTF 10
|||||
Db 32 LVVYPTWTF 41

RESULT 56
US-08-463-160B-68
; Sequence 68, Application US/08463160B
; Patent No. 6172039
; GENERAL INFORMATION:
; APPLICANT: De Angelo, Joseph
; APPLICANT: Motwani, Nalini

APPLICANT: Bajwa, Wajeeh
TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HEMOGLOBIN
TITLE OF INVENTION: AND HEMOGLOBIN VARIANTS IN YEAST
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,160B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/368,407
FILING DATE: 29-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/876,290
FILING DATE: 29-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/684,611
FILING DATE: 12-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Flintoft, Gerald J.
REGISTRATION NUMBER: 20,823
REFERENCE/DOCKET NUMBER: 6666-044-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-463-160B-68

Query Match 100.0%; Score 10; DB 4; length 146;
Best local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPTWTF 10
DB 32 LVVYPTWTF 41

RESULT 57
US-08-463-160B-69
Sequence 69, Application US/08463160B
Patent No. 6172039
GENERAL INFORMATION:
APPLICANT: De Angelo, Joseph
APPLICANT: Motwani, Nalini
APPLICANT: Bajwa, Wajeeh
TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HEMOGLOBIN
TITLE OF INVENTION: AND HEMOGLOBIN VARIANTS IN YEAST
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA

ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,160B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/368,407
FILING DATE: 29-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/876,290
FILING DATE: 29-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/684,611
FILING DATE: 12-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Flintoft, Gerald J.
REGISTRATION NUMBER: 20,823
REFERENCE/DOCKET NUMBER: 6666-044-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-463-160B-69

Query Match 100.0%; Score 10; DB 4; length 146;
Best local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPTWTF 10
DB 32 LVVYPTWTF 41

RESULT 58
US-08-463-160B-71
Sequence 71, Application US/08463160B
Patent No. 6172039
GENERAL INFORMATION:
APPLICANT: De Angelo, Joseph
APPLICANT: Motwani, Nalini
APPLICANT: Bajwa, Wajeeh
TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HEMOGLOBIN
TITLE OF INVENTION: AND HEMOGLOBIN VARIANTS IN YEAST
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,160B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/368,407
FILING DATE: 29-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/876,290
FILING DATE: 29-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/684,611
FILING DATE: 12-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Flintoft, Gerald J.
REGISTRATION NUMBER: 20,823
REFERENCE/DOCKET NUMBER: 6666-044-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-463-160B-71

Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTFORF 10
DB 32 LVVYPWTFORF 41

RESULT 59
US-09-058-562-19
Sequence 19, Application US/09058562A
Patent No. 6184356
GENERAL INFORMATION:
APPLICANT: Anderson, David C.
APPLICANT: Mathews, Antony James
APPLICANT: Stetler, Gary L.
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC HEMOGLOBINS
FILE REFERENCE: BXTB 2087
CURRENT APPLICATION NUMBER: US/09/058,562A
CURRENT FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: US 08/240,712
PRIOR FILING DATE: 1994-05-09
PRIOR APPLICATION NUMBER: PCT/US92/09752
PRIOR FILING DATE: 1993-05-13
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 146
TYPE: PRT
ORGANISM: Human hemoglobin
US-09-058-562-19

Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTFORF 10
DB 32 LVVYPWTFORF 41

RESULT 60
US-09-058-562-20
Sequence 20, Application US/09058562A

Patent No. 6184356
GENERAL INFORMATION:
APPLICANT: Anderson, David C.
APPLICANT: Mathews, Antony James
APPLICANT: Stetler, Gary L.
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC HEMOGLOBINS
FILE REFERENCE: BXTB 2087
CURRENT APPLICATION NUMBER: US/09/058,562A
CURRENT FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: US 08/240,712
PRIOR FILING DATE: 1994-05-09
PRIOR APPLICATION NUMBER: PCT/US92/09752
PRIOR FILING DATE: 1993-05-13
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 146
TYPE: PRT
ORGANISM: Human hemoglobin
US-09-053-562-20

Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTFORF 10
DB 32 LVVYPWTFORF 41

RESULT 61
US-09-053-562-22
Sequence 22, Application US/09058562A
Patent No. 6184356
GENERAL INFORMATION:
APPLICANT: Anderson, David C.
APPLICANT: Mathews, Antony James
APPLICANT: Stetler, Gary L.
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC HEMOGLOBINS
FILE REFERENCE: BXTB 2087
CURRENT APPLICATION NUMBER: US/09/058,562A
CURRENT FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: US 08/240,712
PRIOR FILING DATE: 1994-05-09
PRIOR APPLICATION NUMBER: PCT/US92/09752
PRIOR FILING DATE: 1993-05-13
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
LENGTH: 146
TYPE: PRT
ORGANISM: Human hemoglobin
US-09-058-562-22

Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTFORF 10
DB 32 LVVYPWTFORF 41

RESULT 62
US-09-058-562-26
Sequence 26, Application US/09058562A
Patent No. 6184356
GENERAL INFORMATION:
APPLICANT: Anderson, David C.
APPLICANT: Mathews, Antony James
APPLICANT: Stetler, Gary L.

;; TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC HEMOGLOBINS
;; FILE REFERENCE: BXTB 2087
;; CURRENT APPLICATION NUMBER: US/09/058,562A
;; CURRENT FILING DATE: 1998-04-13
;; PRIOR APPLICATION NUMBER: US 08/240,712
;; PRIOR FILING DATE: 1994-05-09
;; PRIOR APPLICATION NUMBER: PCT/US92/09752
;; PRIOR FILING DATE: 1993-05-13
;; NUMBER OF SEQ. ID NOS: 33
;; SOFTWARE: Patentin Ver. 2.1
;; SEQ ID NO 26
;; LENGTH: 146
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: beta globin
;; US-09-058-562-26

Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LVVYPTWTF 10
Db 32 LVVYPTWTF 41

RESULT 63
; Sequence 2, Application US/09031361
; Patent No. 6204009
; GENERAL INFORMATION:
; APPLICANT: Olson, John S.
; APPLICANT: Mathews, Antony J.
; APPLICANT: Aitken, Jacqueline F.
; APPLICANT: Nagai, Kiyoshi
; TITLE OF INVENTION: Mutant Recombinant Hemoglobins
; TITLE OF INVENTION: Containing Heme Pocket Mutations
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Somatogen, Inc.
; STREET: 2545 Central Avenue, Suite FDI
; CITY: Boulder
; STATE: Colorado
; ZIP: 80301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7.0.1
; SOFTWARE: Microsoft Word 5.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/031,361
; FILING DATE: 26-FEB-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/381,175
; FILING DATE: 30-JAN-1995
; APPLICATION NUMBER: 08/158,483
; FILING DATE: 29-NOV-1993
; APPLICATION NUMBER: 07/443,950
; FILING DATE: 12-DEC-1989
; APPLICATION NUMBER: 07/194,338
; FILING DATE: 16-MAY-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Theresa A.
; REGISTRATION NUMBER: 32547
; REFERENCE/DOCKET NUMBER: 221 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-541-3324
; TELEFAX: 303-444-3013
; INFORMATION FOR SEQ ID NO: 2:

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 146
;; TYPE: amino acid
;; TOPOLOGY: unknown to applicant
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: no
;; US-09-031-361-2

Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LVVYPTWTF 10
Db 32 LVVYPTWTF 41

RESULT 64
; US-08-483-502-10
; Sequence 10, Application US/08483502
; Patent No. 6284492
; GENERAL INFORMATION:
; APPLICANT: Dawson, Jon
; APPLICANT: Grantam, William O.
; APPLICANT: Turpen, Thomas H.
; APPLICANT: Turpen, Ann Myers
; APPLICANT: Garger, Stephen J.
; APPLICANT: Grill, Laurence K.
; TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,502
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/739,143
; FILING DATE:
; APPLICATION NUMBER: US 600,244
; FILING DATE: 22-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 641,617
; FILING DATE: 16-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 310,881
; FILING DATE: 17-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 160,766
; FILING DATE: 26-FEB-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 160,771
; FILING DATE: 26-FEB-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 347,637
; FILING DATE: 05-MAY-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 363,138
; FILING DATE: 08-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 219,279

FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 18604-090574
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-502-10

Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
|||||
DB 32 LVVYPWTQRF 41

RESULT 65
US-09-352-078-1
Sequence 1, Application US/09352078
Patent No. 6337314
GENERAL INFORMATION:
APPLICANT: Theragem, Inc.
APPLICANT: Hoffman, Brian F.
APPLICANT: Dubnick, Bernard
TITLE OF INVENTION: USE OF MAMMALIAN-DERIVED PEPTIDES FOR
FILE REFERENCE: 1944/1D999051
CURRENT APPLICATION NUMBER: US/09/352,078
CURRENT FILING DATE: 1999-07-14
EARLIER APPLICATION NUMBER: PCT/US98/16746
EARLIER FILING DATE: 1998-08-10
EARLIER APPLICATION NUMBER: 60/061,454
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 146
TYPE: PRT
ORGANISM: Homo sapiens
US-09-352-078-1

Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
|||||
DB 32 LVVYPWTQRF 41

RESULT 66
US-08-983-564A-33
Sequence 33, Application US/08983564A
Patent No. 6344600
GENERAL INFORMATION:
APPLICANT: Mercol, Bertrand
APPLICANT: Dierck, Wilfrid
APPLICANT: Lenee, Philippe
APPLICANT: Marden, Michael
APPLICANT: Gruber, Veronique
APPLICANT: Pagnier, Renee-Jossee
APPLICANT: Baudino, Sylvie

APPLICANT: Poyart, Claude
TITLE OF INVENTION: METHOD FOR PRODUCING HARMIN PROTEINS USING PLANT CELLS,
TITLE OF INVENTION: RESULTING PROTEINS AND PRODUCTS CONTAINING SAME
FILE REFERENCE: 8076.147USMO
CURRENT APPLICATION NUMBER: US/08/983,564A
CURRENT FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: PCT/FR96/01123
PRIOR FILING DATE: 1996-07-17
PRIOR APPLICATION NUMBER: 95/08615
PRIOR FILING DATE: 1995-07-17
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 33
LENGTH: 146
TYPE: PRT
ORGANISM: Homo sapiens
US-08-983-564A-33

Query Match 100.0%; Score 10; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
|||||
DB 32 LVVYPWTQRF 41

RESULT 67
PCT-US92-09752-19
Sequence 19, Application PC/TUS9209752
GENERAL INFORMATION:
APPLICANT: ANDERSON, DAVID C.
APPLICANT: MATHEWS, ANTONY JAMES
APPLICANT: SPETTLER, GARY L.
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Broadway and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
Z..P: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09752
FILING DATE: 19930109
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IYER P
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: ANDERSON-6-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US92-09752-19

Query Match 100.0%; Score 10; DB 5; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTORF 10
Db 32 LVVYPWTORF 41

RESULT 68

PCT-US92-09752-20

Sequence 20, Application PC/TUS9209752

GENERAL INFORMATION:

APPLICANT: ANDERSON, DAVID C.

APPLICANT: MATHEWS, ANTONY JAMES

APPLICANT: STELLER, GARY L.

TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Browdy and Neimark

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/09752

FILING DATE: 19930109

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: COOPER, IVER P

REGISTRATION NUMBER: 28,005

REFERENCE/DOCKET NUMBER: ANDERSON-6-PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 146 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

PCT-US92-09752-20

Query Match 100.0%; Score 10; DB 5; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTORF 10
Db 32 LVVYPWTORF 41

RESULT 69

PCT-US92-09752-21

Sequence 21, Application PC/TUS9209752

GENERAL INFORMATION:

APPLICANT: ANDERSON, DAVID C.

APPLICANT: MATHEWS, ANTONY JAMES

APPLICANT: STELLER, GARY L.

TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Browdy and Neimark

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/09752

FILING DATE: 19930109

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: COOPER, IVER P

REGISTRATION NUMBER: 28,005

REFERENCE/DOCKET NUMBER: ANDERSON-6-PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 146 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

PCT-US92-09752-21

Query Match 100.0%; Score 10; DB 5; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTORF 10
Db 32 LVVYPWTORF 41

RESULT 70

PCT-US92-09752-22

Sequence 22, Application PC/TUS9209752

GENERAL INFORMATION:

APPLICANT: ANDERSON, DAVID C.

APPLICANT: MATHEWS, ANTONY JAMES

APPLICANT: STELLER, GARY L.

TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Browdy and Neimark

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/09752

FILING DATE: 19930109

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: COOPER, IVER P

REGISTRATION NUMBER: 28,005

REFERENCE/DOCKET NUMBER: ANDERSON-6-PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US92-09752-22

Query Match 100.0%; Score 10; DB 5; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
DB 32 LVVYPWTQRF 41

RESULT 71
PCT-US92-09752-23

Sequence 23, Application PC/TUS9209752
GENERAL INFORMATION:
APPLICANT: ANDERSON, DAVID C.
APPLICANT: MATHEWS, ANTONY JAMES
APPLICANT: STETLER, GARY L.
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Broadway and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09752
FILING DATE: 19930109
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: ANDERSON-6-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US92-09752-23

Query Match 100.0%; Score 10; DB 5; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
DB 32 LVVYPWTQRF 41

RESULT 72
PCT-US92-09752-24

Sequence 24, Application PC/TUS9209752
GENERAL INFORMATION:
APPLICANT: ANDERSON, DAVID C.
APPLICANT: MATHEWS, ANTONY JAMES
APPLICANT: STETLER, GARY L.
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Broadway and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09752
FILING DATE: 19930109
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: ANDERSON-6-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US92-09752-24

Query Match 100.0%; Score 10; DB 5; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
DB 32 LVVYPWTQRF 41

RESULT 73
PCT-US92-09752-28

Sequence 28, Application PC/TUS9209752
GENERAL INFORMATION:
APPLICANT: ANDERSON, DAVID C.
APPLICANT: MATHEWS, ANTONY JAMES
APPLICANT: STETLER, GARY L.
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Broadway and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09752
FILING DATE: 19930109
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: ANDERSON-6-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US92-09752-28

Query Match
Best Local Similarity 100.0%; Score 10; DB 5; Length 146;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
DB 32 LVVYPWTQRF 41

RESULT 74
US-08-550-715-11
Sequence 11, Application US/08550715
Patent No. 5750345
GENERAL INFORMATION:
APPLICANT: Bowie, Lemuel J.
TITLE OF INVENTION: Human α -Thalassemia Mutations as a Predictor of
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/550,715
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28493/32834
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 147 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-550-715-11

Query Match
Best Local Similarity 100.0%; Score 10; DB 1; Length 147;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
DB 33 LVVYPWTQRF 42

RESULT 75
US-09-230-603-14
Sequence 14, Application US/09230603
Patent No. 6171826
GENERAL INFORMATION:
APPLICANT: LEVINE, JOSEPH D
APPLICANT: APOSTOL, IZYDOR A
TITLE OF INVENTION: METHODS OF CONTROLLING BETA DIMER FORMATION IN
FILE REFERENCE: BXTB3060
CURRENT APPLICATION NUMBER: US/09/230,603
CURRENT FILING DATE: 1999-05-14
EARLIER APPLICATION NUMBER: PCT/US97/13564
EARLIER FILING DATE: 1997-08-01
EARLIER APPLICATION NUMBER: 60/023,211
EARLIER FILING DATE: 1996-08-02
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 147
TYPE: PRT
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: NON_TER
LOCATION: (1)
OTHER INFORMATION: the N-terminal methionine residue incorporated
OTHER INFORMATION: during the translation initiation step is excised
OTHER INFORMATION: during translation and is not present in the
OTHER INFORMATION: mature polypeptide chain
US-09-230-603-14

Query Match
Best Local Similarity 100.0%; Score 10; DB 4; Length 147;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
DB 33 LVVYPWTQRF 42

RESULT 76
US-09-230-603-15
Sequence 15, Application US/09230603
Patent No. 6171826
GENERAL INFORMATION:
APPLICANT: LEVINE, JOSEPH D
APPLICANT: APOSTOL, IZYDOR A
TITLE OF INVENTION: METHODS OF CONTROLLING BETA DIMER FORMATION IN
FILE REFERENCE: BXTB3060
CURRENT APPLICATION NUMBER: US/09/230,603
CURRENT FILING DATE: 1999-05-14
EARLIER APPLICATION NUMBER: PCT/US97/13564
EARLIER FILING DATE: 1997-08-01
EARLIER APPLICATION NUMBER: 60/023,211
EARLIER FILING DATE: 1996-08-02
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 147

TYPE: PRT
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: NON_TER
LOCATION: (1)
OTHER INFORMATION: the N-terminal methionine residue incorporated
OTHER INFORMATION: during the translation initiation step is excised
OTHER INFORMATION: during translation and is not present in the
OTHER INFORMATION: mature polypeptide chain
US-09-230-603-15

Query Match 100.0%; Score 10; DB 4; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVYPWTORE 10
|||
Db 33 LVVYPWTORE 42

RESULT 77
US-09-230-603-16
Sequence 16, Application US/09230603
Patent No. 6171826
GENERAL INFORMATION:
APPLICANT: LEVINE, JOSEPH D
APPLICANT: APOSTOL, IZDOR A
TITLE OF INVENTION: METHODS OF CONTROLLING BETA DIMER FORMATION IN
TITLE OF INVENTION: HEMOGLOBIN
FILE REFERENCE: BXB3060
CURRENT APPLICATION NUMBER: US/09/230, 603
CURRENT FILING DATE: 1999-05-14
EARLIER APPLICATION NUMBER: PCT/US97/13564
EARLIER FILING DATE: 1997-08-01
EARLIER APPLICATION NUMBER: 60/023, 211
EARLIER FILING DATE: 1996-08-02
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 147
TYPE: PRT
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: NON_TER
LOCATION: (1)
OTHER INFORMATION: the N-terminal methionine residue incorporated
OTHER INFORMATION: during the translation initiation step is excised
OTHER INFORMATION: during translation and is not present in the
OTHER INFORMATION: mature polypeptide chain
US-09-230-603-16

Query Match 100.0%; Score 10; DB 4; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVYPWTORE 10
|||
Db 33 LVVYPWTORE 42

RESULT 78
US-09-230-603-18
Sequence 18, Application US/09230603
Patent No. 6171826
GENERAL INFORMATION:
APPLICANT: LEVINE, JOSEPH D
APPLICANT: APOSTOL, IZDOR A
TITLE OF INVENTION: METHODS OF CONTROLLING BETA DIMER FORMATION IN
TITLE OF INVENTION: HEMOGLOBIN
FILE REFERENCE: BXB3060
CURRENT APPLICATION NUMBER: US/09/230, 603

CURRENT FILING DATE: 1999-05-14
EARLIER APPLICATION NUMBER: PCT/US97/13564
EARLIER FILING DATE: 1997-08-01
EARLIER APPLICATION NUMBER: 60/023, 211
EARLIER FILING DATE: 1996-08-02
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 147
TYPE: PRT
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: NON_TER
LOCATION: (1)
OTHER INFORMATION: the N-terminal methionine residue incorporated
OTHER INFORMATION: during the translation initiation step is excised
OTHER INFORMATION: during translation and is not present in the
OTHER INFORMATION: mature polypeptide chain
US-09-230-603-18

Query Match 100.0%; Score 10; DB 4; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVYPWTORE 10
|||
Db 33 LVVYPWTORE 42

RESULT 79
US-09-230-603-19
Sequence 19, Application US/09230603
Patent No. 6171826
GENERAL INFORMATION:
APPLICANT: LEVINE, JOSEPH D
APPLICANT: APOSTOL, IZDOR A
TITLE OF INVENTION: METHODS OF CONTROLLING BETA DIMER FORMATION IN
TITLE OF INVENTION: HEMOGLOBIN
FILE REFERENCE: BXB3060
CURRENT APPLICATION NUMBER: US/09/230, 603
CURRENT FILING DATE: 1999-05-14
EARLIER APPLICATION NUMBER: PCT/US97/13564
EARLIER FILING DATE: 1997-08-01
EARLIER APPLICATION NUMBER: 60/023, 211
EARLIER FILING DATE: 1996-08-02
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 147
TYPE: PRT
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: NON_TER
LOCATION: (1)
OTHER INFORMATION: the N-terminal methionine residue incorporated
OTHER INFORMATION: during the translation initiation step is excised
OTHER INFORMATION: during translation and is not present in the
OTHER INFORMATION: mature polypeptide chain
US-09-230-603-19

Query Match 100.0%; Score 10; DB 4; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVYPWTORE 10
|||
Db 33 LVVYPWTORE 42

RESULT 80
US-09-058-562-21

; Sequence 21, Application US/09058562A
; Patent No. 6184356
; GENERAL INFORMATION:
; APPLICANT: Anderson, David C.
; APPLICANT: Mathews, Antony James
; APPLICANT: Stetler, Gary L.
; TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC HEMOGLOBINS
; FILE REFERENCE: BXTB 2087
; CURRENT APPLICATION NUMBER: US/09/058,562A
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 08/240,712
; PRIOR FILING DATE: 1994-05-09
; PRIOR APPLICATION NUMBER: PCT/US92/09752
; PRIOR FILING DATE: 1993-05-13
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 21
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Human hemoglobin
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (75)
; OTHER INFORMATION: Xaa= Ile or Thr
; US-09-058-562-21

Query Match 100.0%; Score 10; DB 4; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTORF 10
DB 32 LVVYPWTORF 41

RESULT 81
US-08-627-173-5
; Sequence 5, Application US/08627173
; Patent No. 5861483
; GENERAL INFORMATION:
; APPLICANT: TSYRLOVA, IRENA
; APPLICANT: MOLPE, STEPHEN D.
; TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHAYE P. C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,173
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/535,882
; FILING DATE: 28-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 1331-177
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-627-173-5

Query Match 90.0%; Score 9; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTOR 9
DB 1 LVVYPWTOR 9

RESULT 82
US-08-535-882A-5
; Sequence 5, Application US/08535882A
; Patent No. 5939391
; GENERAL INFORMATION:
; APPLICANT: TSYRLOVA, IRENA
; APPLICANT: MOLPE, STEPHEN D.
; TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHAYE P. C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,882A
; FILING DATE: 28-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 1331-177
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-535-882A-5

Query Match 90.0%; Score 9; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTOR 9
DB 1 LVVYPWTOR 9

RESULT 83
US-09-005-546-5
; Sequence 5, Application US/09005546

Patent No. 6090782
GENERAL INFORMATION:
APPLICANT: TSYRLOVA, IRENA
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,546
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/535,882
FILING DATE: 28-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1331-177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-005-546-5

Query Match 90.0%; Score 9; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVYYPWTOR 9
|||
Db 1 LVYYPWTOR 9

RESULT 84
US-08-627-173-20
Sequence 20, Application US/08627173
Patent No. 5861483
GENERAL INFORMATION:
APPLICANT: TSYRLOVA, IRENA
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,173
FILING DATE: 03-APR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/535,882
FILING DATE: 28-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1331-177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-627-173-20

Query Match 90.0%; Score 9; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVYYPWTOR 9
|||
Db 32 LVYYPWTOR 40

RESULT 85
US-08-535-882A-20
Sequence 20, Application US/08535882A
Patent No. 5939391
GENERAL INFORMATION:
APPLICANT: TSYRLOVA, IRENA
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,882A
FILING DATE: 28-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1331-177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-535-882A-20

Query Match 90.0%; Score 9; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTOR 9
| | | | | | | |
DB 32 LVVYPWTOR 40

RESULT 86
US-08-316-424A-6
Sequence 6, Application US/08316424A
Patent No. 6022848
GENERAL INFORMATION:
APPLICANT: KOZLOV, VLADIMIR
APPLICANT: TSYRLOVA, IRENA
TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,424A
FILING DATE: 30-SEP-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1331-122
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEO ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-316-424A-6

Query Match 90.0%; Score 9; DB 3; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTOR 9
| | | | | | | |
DB 32 LVVYPWTOR 40

RESULT 87
US-09-005-546-20
Sequence 20, Application US/09005546
Patent No. 6090782
GENERAL INFORMATION:
APPLICANT: TSYRLOVA, IRENA
APPLICANT: WOJPE, STEPHEN D.
TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND

TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,546
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/535,882
FILING DATE: 28-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1331-177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEO ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-005-546-20

Query Match 90.0%; Score 9; DB 3; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTOR 9
| | | | | | | |
DB 32 LVVYPWTOR 40

RESULT 88
US-08-627-173-6
Sequence 6, Application US/08627173
Patent No. 5861483
GENERAL INFORMATION:
APPLICANT: TSYRLOVA, IRENA
APPLICANT: WOJPE, STEPHEN D.
TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,173
FILING DATE: 03-APR-1996
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/535,882
FILING DATE: 28-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1331-177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-627-173-6

Query Match 80.0%; Score 8; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQ 8
| | | | | | | |
DB 1 LVVYPWTQ 8

RESULT 89
US-08-627-173-27
Sequence 27, Application US/08627173
Patent No. 5861483

GENERAL INFORMATION:
APPLICANT: TSYRLOVA, IRENA
APPLICANT: WOLPE, STEPHEN D.
TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESS: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,173
FILING DATE: 03-APR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/535,882
FILING DATE: 28-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1331-177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-627-173-27

Query Match 80.0%; Score 8; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 VVYPWTQR 9
| | | | | | | |
DB 1 VVYPWTQR 8

RESULT 90
US-08-535-882A-6
Sequence 6, Application US/08535882A
Patent No. 5939391

GENERAL INFORMATION:
APPLICANT: TSYRLOVA, IRENA
APPLICANT: WOLPE, STEPHEN D.
TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESS: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,882A
FILING DATE: 28-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1331-177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-535-882A-6

Query Match 80.0%; Score 8; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQ 8
| | | | | | | |
DB 1 LVVYPWTQ 8

RESULT 91
US-08-535-882A-27
Sequence 27, Application US/08535882A
Patent No. 5939391

GENERAL INFORMATION:
APPLICANT: TSYRLOVA, IRENA
APPLICANT: WOLPE, STEPHEN D.
TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHVE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,882A
FILING DATE: 28-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1331-177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ. ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-535-882A-27

Query Match 80.0%; Score 8; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVVYPTQ 9
DB 1 LVVYPTQ 8

RESULT 92
US-09-005-546-6
Sequence 6, Application US/09005546
Patent No. 6090782
GENERAL INFORMATION:
APPLICANT: TSYRLOVA, IRENA
TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHVE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,546
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/535,882
FILING DATE: 28-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1331-177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ. ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-005-546-6

Query Match 80.0%; Score 8; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPTQ 8
DB 1 LVVYPTQ 8

RESULT 93
US-09-005-546-27
Sequence 27, Application US/09005546
Patent No. 6090782
GENERAL INFORMATION:
APPLICANT: TSYRLOVA, IRENA
TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHVE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,546
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/535,882
FILING DATE: 28-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1331-177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ. ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-005-546-27

Query Match 80.0%; Score 8; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VVYPWTOR 9
|||||||
Db 1 VVYPWTOR 8

RESULT 94

US-08-627-173-7
; Sequence 7, Application US/08627173
; Patent No. 5861483
; GENERAL INFORMATION:
; APPLICANT: TSYRLOVA, IRENA
; APPLICANT: WOJPE, STEPHEN D.
; TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHAYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,173
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/535,882
; FILING DATE: 28-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 1331-177
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-627-173-7

Query Match 70.0%; Score 7; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWT 7
|||||||
Db 1 LVVYPWT 7

RESULT 95

US-08-627-173-10
; Sequence 10, Application US/08627173
; Patent No. 5861483
; GENERAL INFORMATION:
; APPLICANT: TSYRLOVA, IRENA
; APPLICANT: WOJPE, STEPHEN D.
; TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHAYE P.C.

STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,173
FILING DATE: 03-APR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/535,882
FILING DATE: 28-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1331-177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-627-173-10

Query Match 70.0%; Score 7; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VVYPWTQ 8
|||||||
Db 1 VVYPWTQ 7

RESULT 96

US-08-627-173-11
; Sequence 11, Application US/08627173
; Patent No. 5861483
; GENERAL INFORMATION:
; APPLICANT: TSYRLOVA, IRENA
; APPLICANT: WOJPE, STEPHEN D.
; TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHAYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,173
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/535,882
; FILING DATE: 28-SEP-1995
; ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1331-177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-627-173-11

Query Match 70.0%; Score 7; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YPWTQRF 10
Db 1 YPWTQRF 7

RESULT 97
US-08-535-882A-7
Sequence 7, Application US/08535882A
Patent No. 5939391
GENERAL INFORMATION:
APPLICANT: TSYRLOVA, IRENA
TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESSES:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,882A
FILING DATE: 28-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1331-177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-535-882A-7

Query Match 70.0%; Score 7; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWT 7

Db 1 LVVYPWT 7

RESULT 98
US-08-535-882A-10
Sequence 10, Application US/08535882A
Patent No. 5939391
GENERAL INFORMATION:
APPLICANT: TSYRLOVA, IRENA
TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESSES:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,882A
FILING DATE: 28-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1331-177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-535-882A-10

Query Match 70.0%; Score 7; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VVYPWTQ 8
Db 1 VVYPWTQ 7

RESULT 99
US-08-535-882A-11
Sequence 11, Application US/08535882A
Patent No. 5939391
GENERAL INFORMATION:
APPLICANT: TSYRLOVA, IRENA
TITLE OF INVENTION: INHIBITOR OF STEM CELL PROLIFERATION AND
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESSES:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

Query Match 70.0%; Score 7; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWT 7

Search completed: July 1, 2002, 12:06:49
Job time: 22 sec

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,882A
FILING DATE: 28-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1331-177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-535-882A-11

Query Match 70.0%; Score 7; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YPWTQRF 10
|||||||
Db 1 YPWTQRF 7

RESULT 100
US-08-981-384-1
Sequence 1, Application US/08981384
Patent No. 6046168
GENERAL INFORMATION:
APPLICANT: Kagawa, Kyoichi
APPLICANT: Fukuhama, Chizuko
APPLICANT: Matsutaka, Hisako
APPLICANT: Nakamura, Toyoo
APPLICANT: Numata, Masahiro
APPLICANT: Matanabe, Shigeaki
APPLICANT: Honda, Kazuhisa
TITLE OF INVENTION: A peptide inhibiting elevations of triglycerides in
TITLE OF INVENTION: blood and an agent for inhibiting elevations of
TITLE OF INVENTION: triglyceride levels in blood comprising the peptide as
FILE REFERENCE: 382.1016
CURRENT APPLICATION NUMBER: US/08/981,384
CURRENT FILING DATE: 1997-12-23
EARLIER APPLICATION NUMBER: PCT/JP95/01264
EARLIER FILING DATE: 1995-06-23
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 7
TYPE: PRT
ORGANISM: Bos frontalis
US-08-981-384-1

Query Match 70.0%; Score 7; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWT 7
|||||||
Db 1 LVVYPWT 7

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 1, 2002, 12:06:27 ; Search time 14.54 Seconds
(without alignments)
66.086 Million cell updates/sec

Title: US-09-147-490-1
Perfect score: 10
Sequence: 1 LVVYPWTQRF 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283138 segs, 96089334 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : PIR-71:*
1: plr1:*
2: plr2:*
3: plr3:*
4: plr4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	100.0	61	4	TE5317
2	10	100.0	61	4	I52502
3	10	100.0	110	4	I46172
4	10	100.0	122	2	A05304
5	10	100.0	141	1	HGTC
6	10	100.0	141	1	HMF
7	10	100.0	141	1	HSHCR
8	10	100.0	142	1	HSHC
9	10	100.0	145	1	HBOB
10	10	100.0	145	1	HBOB
11	10	100.0	145	1	HBOB
12	10	100.0	145	1	HBOB
13	10	100.0	145	1	HBOB
14	10	100.0	145	1	HBOB
15	10	100.0	145	1	HBOB
16	10	100.0	145	1	HBOB
17	10	100.0	145	1	HBOB
18	10	100.0	145	1	HBOB
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27	10	100.0	145	1	HBOB
28	10	100.0	145	1	HBOB
29	10	100.0	145	1	HBOB

30	10	100.0	146	1	HBOC	hemoglobin beta ch
31	10	100.0	146	1	HBMK	hemoglobin beta ch
32	10	100.0	146	1	HBBM	hemoglobin beta ch
33	10	100.0	146	1	HBBM	hemoglobin beta ch
34	10	100.0	146	1	HBBM	hemoglobin beta ch
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37	10	100.0	146	1	HBBM	hemoglobin beta ch
38	10	100.0	146	1	HBBM	hemoglobin beta ch
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53	10	100.0	146	1	HBBM	hemoglobin beta ch
54	10	100.0	146	1	HBBM	hemoglobin beta ch
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79	10	100.0	146	1	HBBM	hemoglobin beta ch
80	10	100.0	146	1	HBBM	hemoglobin beta ch
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83	10	100.0	146	1	HBBM	hemoglobin beta ch
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86	10	100.0	146	1	HBBM	hemoglobin beta ch
87	10	100.0	146	1	HBBM	hemoglobin beta ch
88	10	100.0	146	1	HBBM	hemoglobin beta ch
89	10	100.0	146	1	HBBM	hemoglobin beta ch
90	10	100.0	146	1	HBBM	hemoglobin beta ch
91	10	100.0	146	1	HBBM	hemoglobin beta ch
92	10	100.0	146	1	HBBM	hemoglobin beta ch
93	10	100.0	146	1	HBBM	hemoglobin beta ch
94	10	100.0	146	1	HBBM	hemoglobin beta ch
95	10	100.0	146	1	HBBM	hemoglobin beta ch
96	10	100.0	146	1	HBBM	hemoglobin beta ch
97	10	100.0	146	1	HBBM	hemoglobin beta ch
98	10	100.0	146	1	HBBM	hemoglobin beta ch
99	10	100.0	146	1	HBBM	hemoglobin beta ch
100	10	100.0	146	1	HBBM	hemoglobin beta ch

ALIGNMENTS

RESULT 1
165317
hemoglobin delta chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 12-Jul-1996 #sequence_revision 31-Jul-1997 #text_change 20-Apr-2000
C:Accession: 165317
R:LiU, J.Z.: Harano, T.; Lanclos, K.D.; Huismann, T.H.
Biochim. Biophys. Acta 909, 208-212, 1987
A:Title: The beta-delta crossover leading to the beta delta hybrid gene of hemoglobin P-
A:Reference number: 152502; MUID:87299720
A:Accession: 165317
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-61 <LIU>
A:Cross-references: GB:M25661; NID:g183863; PIDN:AAA53154.1; PID:g183864
C:Genetics:
A:Note: This sequence was not determined in this report
C:Genetics:
A:Gene: GDB:HBH
A:Cross-references: GDB:119298
A:Map position: 11p15.5-11p15.5
A:Introns: 31/3

Query Match 100.0%; Score 10; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 9e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTOGRF 10
|||||
DB 33 LVVYPWTOGRF 42

RESULT 2
152502
hemoglobin beta chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 31-Jul-1997 #text_change 20-Apr-2000
C:Accession: 152502
R:LiU, J.Z.: Harano, T.; Lanclos, K.D.; Huismann, T.H.
Biochim. Biophys. Acta 909, 208-212, 1987
A:Title: The beta-delta crossover leading to the beta delta hybrid gene of hemoglobin P-
A:Reference number: 152502; MUID:87299720
A:Accession: 152502
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-61 <LIU>
A:Cross-references: GB:M25660; NID:g183856; PIDN:AAA53153.1; PID:g183857
A:Note: This sequence was not determined in this report
C:Genetics:
A:Gene: GDB:HBH
A:Cross-references: GDB:119297
A:Map position: 11p15.4-11p15.4
A:Introns: 31/3

Query Match 100.0%; Score 10; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 9e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTOGRF 10
|||||
DB 33 LVVYPWTOGRF 42

RESULT 3
146172
hypothetical hemoglobin psi-beta-2 pseudogene - goat (fragment)
C:Species: Capra aegagrus hircus (domestic goat)
C:Date: 21-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 19-May-2000
C:Accession: 146172

R:Cleary, M.L.; Schon, E.A.; Lingrel, J.B.
Cell 26, 181-190, 1981
A:Title: Two related pseudogenes are the result of a gene duplication in the goat bet
A:Reference number: 146172; MUID:82137052
A:Accession: 146172
A:Status: translated from GB/EMBL/DBJ; conceptual translation of pseudogene
A:Molecule type: DNA
A:Residues: 1-110 <CLE>
A:Cross-references: EMBL:V00154; NID:9965; PIDN:CAA23469.1; PID:9966
C:Genetics:
A:Introns: 11/3; 18/3; 29/2; 103/3
C:Keywords: pseudogene

Query Match 100.0%; Score 10; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTOGRF 10
|||||
DB 31 LVVYPWTOGRF 40

RESULT 4
A05304
hemoglobin beta-1 chain - Indian spiny-tailed lizard (tentative sequence) (fragments)
C:Species: Uromastyx hardwickii (Indian spiny-tailed lizard)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Mar-2000
C:Accession: A05304
R:Nagvi, S.; Zaidi, Z.H.; von Bahr-Lindstrom, H.; Carlquist, M.; Jernvall, H.
FEBS Lett. 162, 290-295, 1983
A:Reference number: A91314; MUID:84029159
A:Accession: A05304
A:Molecule type: protein
A:Residues: 1-122 <NAG>
A:Note: The peptides were positioned by homology
C:Superfamily: globin; globin homology
C:Keywords: chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F:3-122/Dmain: globin homology (fragments) <GLB>
F:80/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTOGRF 10
|||||
DB 32 LVVYPWTOGRF 41

RESULT 5
HBGTC
hemoglobin beta-C chain - goat
C:Species: Capra aegagrus hircus (domestic goat)
C:Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 03-Mar-2000
C:Accession: B02396; 146277; A02396
R:Schon, E.A.; Cleary, M.L.; Haynes, J.R.; Lingrel, J.B.
Cell 27, 359-369, 1981
A:Title: Structure and evolution of goat gamma-, beta(c)- and beta(A)-globin genes: t
A:Reference number: A90817; MUID:82137075
A:Accession: B02396
A:Molecule type: DNA
A:Residues: 1-141 <SCH>
A:Cross-references: GB:M15389
A:Note: Initiator Met not shown
R:Haynes, J.R.; Rostock, P.R.; Schon, E.A.; Gallagher, P.M.; Burks, D.J.; Smith, K.;
J. Biol. Chem. 255, 6355-6367, 1980
A:Title: The isolation of the beta-a-, beta-c-, and gamma-globin genes and a presumpt
A:Reference number: 146277; MUID:80227766
A:Accession: 146277
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 66-93,'XX',96-115,'XX',118-134 <HAY>
A:Cross-references: GB:K00662; NID:g164154; PID:g164156
C:Comment: This type of beta-C chain is found when anemia has been experimentally produced
C:Genetics:
A:Introns: 26/2; 100/3
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F:1-141/Domain: globin homology <GLB>
F:58/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:87/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTORE 10
|||||
DB 27 LVVYPWTORE 36

RESULT 6
HBMFC
hemoglobin beta-C chain - mouflon (tentative sequence)
C:Species: Ovis orientalis musimon, Ovis ammon musimon (mouflon)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 03-Mar-2000
C:Accession: A90232; A02396
R:Wilson, J.B.; Miller, A.; Huisman, T.H.J.
Biochem. Genet. 4, 677-688, 1970
A:Title: Production of hemoglobin C in the mouflon (Ovis musimon pallas, 1811) and the plides from the beta(B) and beta (C) chains.
A:Reference number: A90232; MUID:71089262
A:Accession: A90232

A:Molecule type: protein
A:Residues: 1-141 <MII>
A:Note: Compositions of tryptic peptides were determined; positions 100-111 were sequenced
C:Comment: This type of beta-C chain is found when anemia has been experimentally produced
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F:1-141/Domain: globin homology <GLB>
F:58/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:87/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTORE 10
|||||
DB 27 LVVYPWTORE 36

RESULT 7
HBSHC
hemoglobin beta-C chain - aoudad (tentative sequence)
C:Species: Ammotragus leervia (aoudad, Barbary sheep)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 03-Mar-2000
C:Accession: B90232; A02396
R:Wilson, J.B.; Miller, A.; Huisman, T.H.J.
Biochem. Genet. 4, 677-688, 1970
A:Title: Production of hemoglobin C in the mouflon (Ovis musimon pallas, 1811) and the plides from the beta(B) and beta (C) chains.
A:Reference number: A90232; MUID:71089262
A:Accession: B90232

A:Molecule type: protein
A:Residues: 1-141 <MII>
A:Note: Compositions of tryptic peptides were determined; positions 100-111 were sequenced
C:Comment: This type of beta-C chain is found when anemia has been experimentally produced
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F:1-141/Domain: globin homology <GLB>
F:58/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:87/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTORE 10
|||||
DB 27 LVVYPWTORE 36

RESULT 8
HBSHC
hemoglobin beta-C chain - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 30-Sep-1993 #sequence_revision 30-Jan-1998 #text_change 03-Mar-2000
C:Accession: S10074; B92027; A90045; A02396
R:Garner, K.J.; Lingrel, J.B.
J. Mol. Evol. 28, 175-184, 1989
A:Title: A comparison of the beta(A)- and beta(B)-globin gene clusters of sheep.
A:Reference number: S10073; MUID:89178744
A:Accession: S10074

A:Molecule type: DNA
A:Residues: 1-142 <GAP>
A:Cross-references: EMBL:X14728; NID:g1212; PID:CAA32850.1; PID:g1213
A:Note: The authors translated the codon GTC for residue 30 as Ala
A:Note: the sequence of codons and residues 41-60 is repeated twice in the authors' t
R:Boyer, S.H.; Hathaway, P.; Pascasio, F.; Bordley, J.; Orton, C.; Naughton, M.A.
J. Biol. Chem. 242, 2211-2232, 1967
A:Title: Differences in the amino acid sequences of tryptic peptides from three sheep
A:Reference number: A92027; MUID:67134347
A:Accession: B92027

A:Molecule type: protein
A:Residues: 2-64,'B',66-68,'B',70-71,'Z',73-74,'BB',77-82,'Z',84-85,'Z',87-94,'B',96,
A:Experimental source: Dorset breed
R:Wilson, J.B.; Edwards, W.C.; McDaniel, M.; Dobbs, M.M.; Huisman, T.H.J.
Arch. Biochem. Biophys. 115, 385-400, 1966
A:Title: The structure of sheep hemoglobins. II. The amino acid composition of the tr
A:Reference number: A90045
A:Accession: A90045

A:Molecule type: protein
A:Residues: 2-64,'B',66-68,'B',70-71,'Z',73-74,'BB',77-82,'Z',84-85,'Z',87-94,'B',96,
A:Experimental source: Rambouillet breed
A:Note: There are several discrepancies between the sequence in this paper and that g
C:Comment: This beta-C chain is produced when anemia is experimentally induced.
C:Genetics:
A:Introns: 26/2; 100/3
C:Complex: Two beta chains combine to form heterotetramers with two alpha chains to f
C:Function:
A:Description: In erythrocytes binds and transports molecular oxygen from lung to tis
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metallopro
F:1-142/Domain: globin homology <GLB>
F:2-142/Product: hemoglobin beta-C chain #status experimental <MAT>
F:59/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:88/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 142;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTORE 10
|||||
DB 28 LVVYPWTORE 37

RESULT 9
HBSOB
hemoglobin beta chain (validated) - bovine
N:Alternate names: hemoglobin-derived opioid peptide
N:Contains: LVV-hemorphin-7; VV-hemorphin-7

C:Species: Bos primigenius taurus (cattle)
C:Date: 24-Apr-1994 #sequence_revision 25-Feb-1985 #text_change 15-Sep-2000
C:Accession: B93504; A90046; B90046; A90052; B90052; S35636; S65609; A02387
R:Schmehl, J.C.; Duncan, C.H.
Nucleic Acids Res. 12, 1641-1655, 1984
A:Title: Ruminant globin gene structures suggest an evolutionary role for Alu-type repeats
A:Reference number: A93504; MUID:84144058
A:Accession: B93504
A:Molecule type: DNA
A:Residues: 1-145 <SC1>
A:Cross-references: EMBL:X00376; NID:9394; PIDN:CA42511.1; PID:9395
A:Experimental source: beta A allele, Jersey cattle
R:Schroeder, W.A.; Shelton, J.R.; Shelton, J.B.; Robbertson, B.; Babin, D.R.
Arch. Biochem. Biophys. 120, 124-135, 1967
A:Title: A comparison of amino acid sequences in the beta-chains of adult bovine hemoglobin
A:Reference number: A90046; MUID:68001834
A:Accession: A90046
A:Molecule type: protein
A:Residues: 1-145 <SC1>
A:Experimental source: beta A allele, Jersey cattle
A:Accession: B90046
A:Molecule type: protein
A:Residues: 1-14, 'S', '16-17', 'H', '19-118', 'N', '120-145 <SC2>
A:Experimental source: beta B allele, Jersey cattle
R:Schroeder, W.A.; Shelton, J.R.; Shelton, J.B.; Apell, G.; Huisman, T.H.J.; Smith, L.L.
Arch. Biochem. Biophys. 152, 222-232, 1972
A:Title: Amino acid sequences in the beta-chains of adult bovine hemoglobins C-Rhodesia
A:Reference number: A90052; MUID:73007895
A:Accession: A90052
A:Molecule type: protein
A:Residues: 1-130, 'Q', '132-145 <SC3>
A:Experimental source: C-Rhodesia allele, Angoni cattle (East African short-horn zebu)
A:Accession: B90052
A:Molecule type: protein
A:Residues: 1-19, 'G', '21-42', 'T', '44-145 <SC4>
A:Experimental source: D-Zambia allele, Angoni cattle (East African short-horn zebu)
R:Barkhudaryan, N.; Kellermann, J.; Galoyan, A.; Lottspeich, F.
FEBS Lett. 329, 215-218, 1993
A:Title: High molecular weight aspartic endopeptidase generates a coronaro-constrictory
A:Reference number: S35696; MUID:93359052
A:Accession: S35696
A:Molecule type: protein
A:Residues: 31-40 <BAR>
A:Note: LVV-hemorphin-7 acts as a vasoconstrictor
R:Audes-Dutau, I.; Capdevielle, J.; Seris, J.L.; Combes, D.
FEBS Lett. 364, 115-119, 1995
A:Title: Bitter peptide from hemoglobin hydrolysate: isolation and characterization.
A:Reference number: S65609; MUID:95269781
A:Accession: S65609
A:Molecule type: protein
A:Residues: 32-40 <ANB>
A:Note: VV-hemorphin-7 isolated from a hydrolysate has a bitter taste
R:Fernli, G.
submitted to the Brookhaven Protein Data Bank, May 1993
A:Reference number: A52353; PDB:1HDA
A:Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 1-145
R:Perutz, M.F.; Fernli, G.; Poyart, C.; Pagnier, J.; Kister, J.
J. Mol. Biol. 233, 536-545, 1993
A:Title: A novel allosteric mechanism in haemoglobin. Structure of bovine deoxyhaemoglobin
haemoglobin.
A:Reference number: A58463; MUID:94016570
A:Contents: annotation; X-ray crystallography, 2.2 angstroms
C:Genetics:
A:Introns: 28/2; 102/3
C:Function:
A:Description: In erythrocytes binds and transports molecular oxygen from lung to tissue
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotrimer; iron; metalloprotein
F:2-145/Domain: globin homology <GLB>
F:32-40/Product: LVV-hemorphin-7 #status experimental <OPTA>
F:32-40/Product: VV-hemorphin-7 (distal axial ligand) #status predicted
F:62/Binding site:oxygen (His)

```
F:91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match          100.0%; Score 10; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LVVYPWTFGRF 10
        |||
Db       31 LVVYPWTFGRF 40

RESULT 10.
HBBORR
hemoglobin beta-A chain - banteng (tentative sequence)
C:Species: Bos javanicus (banteng)
C>Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 03-Mar-2000
C:Accession: A02388
R:Namikawa, T.; Takemura, O.; Takahashi, K.
Biochem. Genet. 21, 787-796, 1983
A>Title: Hemoglobin Bali (bovine); beta(A)18(B1)Lys -> His: one of the "missing links
A:Reference number: A02388; MUID:84023669
A:Accession: A02388
A:Molecule type: protein
A:Residues: 1-145 <NMA>
A:Experimental source: Hereford breed
A>Note: Cyclic peptides were positioned by homology with the bovine sequence
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen car
F:2-145/Dmain: globin homology <GLB>
F:62/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:91/Binding site: heme iron (His) (proximal axial ligand) #status predicted
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Query Match 100.0%; Score 10; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTORF 10
   |||||
DB 31 LVVYPWTORF 40

RESULT 11
HBBOG
hemoglobin beta chain - gayal
C:Species: Bos gaurus frontalis (gayal)
C:Idate: 17-May-1985 #sequence_revision 17-May-1985 #text_change 03-Mar-2000
C:Accession: A02389
R:Lalthantluanga, R.; Braunitzer, G.
Hoppe-Seyler's Z. Physiol. Chem. 365, 737-741, 1984
A:Title: Amino-acid sequence of gayal hemoglobin (Bos gaurus frontalis, Bovidae).
A:Reference number: A91737; MUID:65005246
A:Accession: A02389
A:Molecule type: protein
A:Residues: 1-145 <LAL>
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen car
F:2-145/Domain: globin homology <GLB>
F:62/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTORF 10
   |||||
DB 31 LVVYPWTORF 40

RESULT 12
HBBOG
hemoglobin beta chain - gayal
C:Species: Bos gaurus frontalis (gayal)
C:Idate: 17-May-1985 #sequence_revision 17-May-1985 #text_change 03-Mar-2000
C:Accession: A02389
R:Lalthantluanga, R.; Braunitzer, G.
Hoppe-Seyler's Z. Physiol. Chem. 365, 737-741, 1984
A:Title: Amino-acid sequence of gayal hemoglobin (Bos gaurus frontalis, Bovidae).
A:Reference number: A91737; MUID:65005246
A:Accession: A02389
A:Molecule type: protein
A:Residues: 1-145 <LAL>
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen car
F:2-145/Domain: globin homology <GLB>
F:62/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTORF 10
   |||||
DB 31 LVVYPWTORF 40

RESULT 13
HBBOG
hemoglobin beta chain - gayal
C:Species: Bos gaurus frontalis (gayal)
C:Idate: 17-May-1985 #sequence_revision 17-May-1985 #text_change 03-Mar-2000
C:Accession: A02389
R:Lalthantluanga, R.; Braunitzer, G.
Hoppe-Seyler's Z. Physiol. Chem. 365, 737-741, 1984
A:Title: Amino-acid sequence of gayal hemoglobin (Bos gaurus frontalis, Bovidae).
A:Reference number: A91737; MUID:65005246
A:Accession: A02389
A:Molecule type: protein
A:Residues: 1-145 <LAL>
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen car
F:2-145/Domain: globin homology <GLB>
F:62/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

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HBA2

hemoglobin beta chain - yak

C:Species: Bos mutus grunniens (yak)

C:Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 03-Mar-2000

C:Accession: A02390

R:Lalthantlanga, R.; Wiesner, H.; Braunitzer, G.

Biol. Chem. Hoppe-Seyler 366, 63-68, 1985

A:Title: Studies on yak hemoglobin (Bos grunniens, Bovidae): structural basis for high

F:62/Binding site: oxygen (His) (proximal axial ligand) #status predicted

F:91/Binding site: heme iron (His)

A:Reference number: A90689; PMID:85225945

A:Contents: beta-I and beta-II alleles

A:Accession: A02390

A:Molecule type: protein

A:Residues: 1-145 <TR>

A:Note: The sequence from the beta-I allele differs from that shown in having 49-Thr, 11

C:Comment: The beta-II allele is shown.

C:Superfamily: globin; globin occurs much more frequently than the beta-I allele.

C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier

F:2-145/Domain: globin homology <GLB>

F:62/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match

Best Local Similarity 100.0%; Score 10; DB 1; Length 145;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVYPWTORF 10

Db 31 LVVYPWTORF 40

RESULT 13

HBBOKA

hemoglobin beta chain - greater kudu

C:Species: Tragelaphus strepsiceros (greater kudu)

C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 03-Mar-2000

C:Accession: A02391

R:Kodewald, K.; Wiesner, H.; Braunitzer, G.

Biol. Chem. Hoppe-Seyler 366, 395-402, 1985

A:Title: Primary structure of the hemoglobins from the greater Kudu antelope (Tragelaphus

A:Reference number: A90684; PMID:85279893

A:Accession: A02391

A:Molecule type: protein

A:Residues: 1-145 <ROD>

A:Note: there are two alleles for the beta chain, one having the sequence shown and the

C:Superfamily: globin; globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier

F:2-145/Domain: globin homology <GLB>

F:62/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match

Best Local Similarity 100.0%; Score 10; DB 1; Length 145;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVYPWTORF 10

Db 31 LVVYPWTORF 40

RESULT 14

HBBKN

hemoglobin beta chain - European moose

C:Species: Alces alces alces (European moose, elk)

C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 03-Mar-2000

C:Accession: A02392

R:Aschauer, H.; Wiesner, H.; Braunitzer, G.

Hoppe-Seyler's Z. Physiol. Chem. 365, 1323-1330, 1984

A:Title: Zur intrinsischen Sauerstoffaffinität: die Primärstruktur eines weiteren Rumi

A:Reference number: A91729; PMID:85078042

A:Accession: A02392

A:Molecule type: protein

A:Residues: 1-145 <ASC>

C:Superfamily: globin; globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier

F:2-145/Domain: globin homology <GLB>

F:62/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match

Best Local Similarity 100.0%; Score 10; DB 1; Length 145;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVYPWTORF 10

Db 31 LVVYPWTORF 40

RESULT 15

HBBE3

hemoglobin beta-III chain - Virginia white-tailed deer

C:Species: Odocoileus virginianus virginianus (Virginia white-tailed deer)

C:Date: 28-Feb-1986 #sequence_revision 28-Feb-1986 #text_change 03-Mar-2000

C:Accession: A02393

R:Shimizu, K.; Wong, S.C.; Wilson, J.B.; Lam, H.; Reynolds, A.E.; Singh, P.; Huismann,

Hemoglobin 7, 15-45, 1983

A:Title: The primary sequence of the beta chain of Hb type III of the Virginia white-

deer hemoglobins, types II, IV, V, and VII, and relationships between intermolecular

A:Reference number: A02393; PMID:83185439

A:Accession: A02393

A:Molecule type: protein

A:Residues: 1-145 <SHI>

A:Note: This chain is one of five beta chain alleles.

C:Superfamily: globin; globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier

F:2-145/Domain: globin homology <GLB>

F:62/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match

Best Local Similarity 100.0%; Score 10; DB 1; Length 145;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVYPWTORF 10

Db 31 LVVYPWTORF 40

RESULT 16

HBSHB

hemoglobin beta-B chain - sheep

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 24-Apr-1984 #sequence_revision 30-Jan-1998 #text_change 19-May-2000

C:Accession: S10073; A92027; I47082; A02394

R:Boyer, S.H.; Hathaway, P.; Pascasio, F.; Bordley, J.; Orton, C.; Naughton, M.A.

J. Biol. Chem. 247, 2211-2232, 1967

A:Title: Differences in the amino acid sequences of tryptic peptides from three sheep

A:Reference number: S10073; PMID:61134347

A:Accession: S10073

A:Molecule type: DNA

A:Residues: 1-145 <GARL>

A:Cross-references: EMBL:X14727; NID:g1208; PIDN:CAA3849.1; PID:g1209

A:Note: the sequence of codons and residues 44-63 is repeated twice in the authors' t

R:Boyer, S.H.; Hathaway, P.; Pascasio, F.; Bordley, J.; Orton, C.; Naughton, M.A.

J. Biol. Chem. 247, 2211-2232, 1967

A:Title: Differences in the amino acid sequences of tryptic peptides from three sheep

A:Reference number: A92027; PMID:61134347

A:Accession: A92027

A:Molecule type: protein

A:Residues: 1-48, 'B', '50-67', 'B', '69-97', 'B', '99', '102-145 <BOY>

R:Garner, K.J.; Lingrel, J.B.

Mol. Biol. Evol. 5, 134-140, 1988

A:Title: Structural organization of the beta-globin locus of beta-haplotype sheep.
A:Reference number: 147082; MUID:88216150
A:Accession: 147082
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-28 <GNR2>
A:Cross-references: GB:M19754; NID:g165890; PIDN:AAA31528.1; PID:g552420
C:Genetics:
A:introns: 29/2; 103/3
C:Complex: two beta chains combine in heterotetramers with two alpha chains (see PIR:HAS
C:Function:
A:Description: in erythrocytes binds and transports molecular oxygen from lung to tissue
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
F:1-145/Product: hemoglobin beta-B chain #status experimental <MAT>
F:2-145/Domain: globin homology <GLB>
F:62/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10
DB 31 LVVYPTQRF 40

RESULT 17

HBSHA
hemoglobin beta-A chain - sheep (tentative sequence)
C:Species: Ovis orientalis aries; Ovis ammon aries (domestic sheep)
C>Date: 30-Sep-1992 #sequence; revision 30-Sep-1992 #text_change 31-Mar-2000
C:Accession: A94556; A90237; A92306; A02394
R:Beale, D.
submitted to the Atlas, August 1967
A:Reference number: A94556
A:Accession: A94556
A:Molecule type: protein
A:Residues: 1-145 <BEAL>
R:Beale, D.
Biochem. J. 103, 129-140, 1967
A:Title: A partial amino acid sequence for sheep haemoglobin A.
A:Reference number: A90237; MUID:67209244
A:Accession: A90237
A:Molecule type: protein
A:Residues: 1-145 <BEA2>
R:Kreischmer, P.J.; Coon, H.C.; Davis, A.; Harrison, M.; Nienhuis, A.W.
J. Biol. Chem. 256, 1975-1982, 1981
A:Title: Hemoglobin switching in sheep. Isolation of the fetal gamma-globin gene and dem
s DNA.
A:Reference number: A92306; MUID:81117290
A:Accession: A92306
A:Molecule type: DNA
A:Residues: 1-29; 39-56, 'P', 58-59; 72-85; 104-145 <KRE>
A:Cross-references: GB:K02820
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
F:2-145/Domain: globin homology <GLB>
F:62/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10
DB 31 LVVYPTQRF 40

RESULT 18

HBC7A
hemoglobin beta-A chain - goat
C:Species: Capra aegagrus hircus (domestic goat)
C>Date: 18-Aug-1982 #sequence; revision 18-Aug-1982 #text_change 03-Mar-2000
C:Accession: A90817; 146170; 146273; 146274; A92028; A90049; A02395
R:Schon, E.A.; Cleary, M.L.; Haynes, J.R.; Lingrel, J.B.
Cell 27, 359-369, 1981
A:Title: Structure and evolution of goat gamma-, beta(c)- and beta(A)-globin genes: t
A:Reference number: A90817; MUID:82337075
A:Accession: A90817
A:Molecule type: DNA
A:Residues: 1-145 <SCH>
A:Cross-references: GB:M15387; NID:g164133; PIDN:AAA30913.1; PID:g164134
R:Cleary, M.L.; Haynes, J.R.; Schon, E.A.; Lingrel, J.B.
Nucleic Acids Res. 8, 4791-4802, 1980
A:Title: Identification by nucleotide sequence analysis of a goat pseudoglobin gene.
A:Reference number: 146169; MUID:81076616
A:Accession: 146170
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-29 <CLE1>
A:Cross-references: EMBL:V00152; NID:g961; PIDN:CAA23467.1; PID:g962
A:Accession: 146171
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 64-99 <CLE2>
A:Cross-references: EMBL:V00153; NID:g963; PIDN:CAA23468.1; PID:g669075
R:Haynes, J.R.; Rostock, P.R.; Schon, E.A.; Gallagher, P.M.; Burks, D.J.; Smith, K.;
J. Biol. Chem. 255, 6355-6367, 1980
A:Title: The isolation of the beta-a-, beta-c-, and gamma-globin genes and a presumpt
A:Reference number: 146273; MUID:80227766
A:Accession: 146273
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 64-97 <HAY1>
A:Cross-references: GB:K00657; NID:g164128; PIDN:AAA30911.1; PID:g552351
A:Accession: 146274
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 114-119 <HAY2>
A:Cross-references: GB:K00658; NID:g164129; PIDN:AAA30912.1; PID:g552352
R:Huisman, T.H.J.; Adams, H.R.; Dimmock, M.O.; Edwards, W.E.; Wilson, J.B.
J. Biol. Chem. 242, 2534-2541, 1967
A:Title: The structure of goat hemoglobins. I. Structural studies of the beta chains
A:Reference number: A92028; MUID:67165362
A:Accession: A92028
A:Molecule type: protein
A:Residues: 1-145 <HUI>
A:Experimental source: A allele, partial sequence
R:Adams, H.R.; Boyd, E.M.; Wilson, J.B.; Miller, A.; Huisman, T.H.J.
Arch. Biochem. Biophys. 127, 398-405, 1968
A:Title: The structure of goat hemoglobins. III. Hemoglobin D, a beta chain variant w
A:Reference number: A90047; MUID:65036192
A:Accession: A90047
A:Molecule type: protein
A:Residues: 1-19, 'H', '21-145 <ADA>
A:Experimental source: D allele, partial sequence
R:Wrightstone, R.N.; Wilson, J.B.; Miller, A.; Huisman, T.H.J.
Arch. Biochem. Biophys. 138, 451-456, 1970
A:Title: The structure of goat hemoglobins. IV. A third beta chain variant (beta-E) w
A:Reference number: A90049; MUID:70252721
A:Accession: A90049
A:Molecule type: protein
A:Residues: 1-85, 'H', '87-102, 'R', 104-123, 'V', 125-145 <WRI>
A:Experimental source: E allele, partial sequence
C:Comment: The A allele sequence is shown.
C:Genetics:
A:introns: 29/2; 103/3
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen car
F:2-145/Domain: globin homology <GLB>
F:62/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
| | | | | | | | | |
DB 31 LVVYPWTORE 40

RESULT 19

HBBOF hemoglobin beta chain, fetal - bovine

N:Alternate names: hemoglobin gamma chain

C:Species: Bos primigenius taurus (cattle)

C>Date: 24-Apr-1984 #sequence revision 24-Apr-1984 #text_change 03-Mar-2000

C:Accession: A93504; A90549; A02398

R:Schimenti, J.C.; Duncan, C.H.

Nucleic Acids Res. 12, 1641-1655, 1984

A:Title: Ruminant globin gene structures suggest an evolutionary role for Alu-type repeats

A:Reference number: A93504; MUID:84144058

A:Accession: A93504

A:Molecule type: DNA

A:Residues: 1-145 <SCH>

A:Cross-references: GB:X00354; NID:g392; PIDN:CAA25101.1; PID:g393

R:Rabin, D.R.; Schroeder, W.A.; Shelton, J.R.; Shelton, J.B.; Roberson, B.

Biochemistry 5, 1297-1310, 1966

A:Title: The amino acid sequence of the gamma chain of bovine fetal hemoglobin.

A:Reference number: A90549; MUID:67089183

A:Accession: A90549

A:Molecule type: protein

A:Residues: 1-145 <BAB>

C:Genetics:

A:Introns: 29/2; 103/3

C:Superfamily: globin; globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier

F:2-145/Domain: globin homology <GLB>

F:62/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
| | | | | | | | | |
DB 31 LVVYPWTORE 40

RESULT 20

HBGTF

hemoglobin beta chain, fetal - goat

N:Alternate names: hemoglobin gamma chain [mismomer]

C:Species: Capra aegagrus hircus (domestic goat)

C>Date: 18-Aug-1982 #sequence revision 18-Aug-1982 #text_change 03-Mar-2000

C:Accession: A02399; A91710; I46280

R:Schon, E.A.; Cleary, M.L.; Haynes, J.R.; Lingrel, J.E.

Cell 27, 355-369, 1981

A:Title: Structure and evolution of goat gamma-, beta(c)- and beta(A)-globin genes: three

A:Reference number: A90817; MUID:82137075

A:Accession: A02399

A:Molecule type: DNA

A:Residues: 1-145 <SCH>

A:Cross-references: GB:M15388; NID:g164169; PIDN:AAA30925.1; PID:g164170

R:Kleinschmidt, T.; Braunitzer, G.

Hoppe-Seiler's Z. Physiol. Chem. 363, 789-796, 1982

A:Title: Die Primerstruktur der gamma-Ketten der foetalen Haemoglobine von Schaf (Ovis

A:Reference number: A91710; MUID:83005406

A:Accession: A91710

A:Molecule type: protein

A:Residues: 1-145 <KLE>

R:Haynes, J.R.; Rostock, P.R.; Schon, E.A.; Gallagher, P.M.; Burks, D.J.; Smith, K.;

J. Biol. Chem. 255, 6355-6367, 1980

A:Title: The isolation of the beta-a-, beta-c-, and gamma-globin genes and a presumpt

A:Reference number: I46273; MUID:80227766

A:Accession: I46279

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 52-97 <HAV1>

A:Cross-references: GB:K00663; NID:g164164; PIDN:AAA30923.1; PID:g164167

A:Accession: I46280

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 104-118, 'XXX', 122-123, 'G', 125-139 <NAV2>

A:Cross-references: GB:K00664; NID:g164165; PIDN:AAA30924.1; PID:g552354

C:Comment: This is regarded as a beta chain produced by the fetus, not as a gamma cha

C:Superfamily: globin; globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metallopro

F:1-145/Product: hemoglobin beta chain, fetal #status experimental <MAT>

F:2-145/Domain: globin homology <GLB>

F:62/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
| | | | | | | | | |
DB 31 LVVYPWTORE 40

RESULT 21

HGSH

hemoglobin beta chain, fetal - sheep

N:Alternate names: hemoglobin gamma chain [mismomer]

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C>Date: 31-Mar-1992 #sequence revision 31-Mar-1992 #text_change 03-Mar-2000

C:Accession: B92306; S45297; A90610; A92306

R:Kreischmer, P.J.; Coon, H.C.; Davits, A.; Harrison, M.; Nienhuis, A.W.

J. Biol. Chem. 256, 1975-1982, 1981

A:Title: Hemoglobin switching in sheep. Isolation of the fetal gamma-globin gene and

s DNA.

A:Reference number: A92306; MUID:81117290

A:Accession: B92306

A:Molecule type: DNA

A:Residues: 1-29;52-96;104-145 <KRE>

A:Cross-references: GB:K02824; NID:g165901; PIDN:AAA31533.1; PID:g552423; GB:K02825;

R:Saban, J.; King, D.

Biochim. Biophys. Acta 1218, 87-90, 1994

A:Title: Sequence of the sheep fetal beta globin gene and flanking region.

A:Reference number: S45297; MUID:94250699

A:Accession: S45297

A:Molecule type: DNA

A:Residues: 1-17,30-47, 'F',49-145 <SAB>

A:Cross-references: EMBL:U01378; NID:g437113; PIDN:AAA19218.1; PID:g437114

R:Dartre, P.D.; Lehmann, H.

Biochim. Biophys. Acta 446, 10-18, 1976

A:Title: The gamma chain of the lamb.

A:Reference number: A90610; MUID:77022158

A:Accession: A90610

A:Molecule type: protein

A:Residues: 1-118, 'EG',121-145 <DAR>

C:Comment: This is regarded as a beta chain produced by the fetus, not as a gamma cha

C:Genetics:

A:Introns: 17/2; 103/3

C:Complex: Two gamma chains combine in heterotetramers with two alpha chains to form

A:Description: in erythrocytes binds and transports molecular oxygen from placenta to

C:Superfamily: globin; globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metallopro

F:1-145/Product: hemoglobin beta chain, fetal #status experimental <MAT>

F:2-145/Domain: globin homology <GLB>
F:62/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10
|||||
Db 31 LVVYPTQRF 40

RESULT 22

hemoglobin beta chain - domestic water buffalo

C:Species: Bubalus arnee bubalis (domestic water buffalo)

C:Date: 07-Aug-1998 #sequence_revision 07-Aug-1998 #text_change 20-Jun-2000

C:Accession: B58794; A49141

R:Ferranti, P.; Malorni, A.; Marino, G.; Pucci, P.; Di Luccia, A.; Ferrara, L.

Int. J. Mass Spectrom. Ion Process. 111, 287-300, 1991

A:Title: FAB overlapping: a strategy for sequencing homologous proteins.

A:Reference number: A58794

A:Accession: B58794

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-145 <FER>

R:Ferranti, P.; Di Luccia, A.; Marino, G.; Pucci, P.; Di Luccia, A.; Ferrara, L.

Comp. Biochem. Physiol. B 101, 91-98, 1992

A:Title: River buffalo (Bubalus bubalis L.) AA phenotype haemoglobins: characterization

I the primary structure of the constitutive chains by mass spectrometry.

A:Reference number: A49141; MUID:92362189

A:Accession: A49141

A:Molecule type: protein

A:Residues: 1-145 <FER2>

A:Experimental source: AA phenotype

A>Note: sequence extracted from NCBI backbone (NCBIP:111135)

C:Superfamily: globin; globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier

F:2-145/Domain: globin homology <GLB>

F:62/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10
|||||
Db 31 LVVYPTQRF 40

RESULT 23
S13609
hemoglobin beta chain - reindeer
C:Species: Rangifer tarandus (reindeer)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 19-May-2000
C:Accession: S13609
R:Petruzzelli, R.; Barra, D.; Bossa, F.; Condo, S.G.; Brix, O.; Nuutinen, M.; Giardina, B.

Biochim. Biophys. Acta 1076, 221-224, 1991

A:Title: The primary structure of hemoglobin from reindeer (Rangifer tarandus)

A:Reference number: S13481; MUID:91152092

A:Accession: S13609

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-145 <PET>

C:Superfamily: globin; globin homology

C:Keywords: blood; chromoprotein; heme; iron; metalloprotein; oxygen carrier

F:2-145/Domain: globin homology <GLB>

F:62/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10
|||||
Db 31 LVVYPTQRF 40

RESULT 24

hemoglobin beta chain - European bison

C:Species: Bison bonasus (European bison)

C:Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 19-May-2000

C:Accession: C25727

R:Mazur, G.; Muller, E.; Braunitzer, G.; Wiesner, H.

Biol. Chem. Hoppe-Seyler 367, 417-423, 1986

A:Title: Intrinsische Sauerstoffaffinität der Hamoglobine: das Hamoglobin des Wisents

A:Reference number: A90706; MUID:86296178

A:Accession: C25727

A:Molecule type: protein

A:Residues: 1-145 <MAZ>

C:Superfamily: globin; globin homology

C:Keywords: blood; chromoprotein; heme; iron; metalloprotein; oxygen carrier

F:2-145/Domain: globin homology <GLB>

F:62/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:91/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10
|||||
Db 31 LVVYPTQRF 40

RESULT 25

hemoglobin beta chain - pygmy chimpanzee

C:Species: Pan paniscus (pygmy chimpanzee, bonobo)

C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 03-Mar-2000

C:Accession: D93303

R:Goodman, M.; Braunitzer, G.; Stangl, A.; Schrank, B.

Nature 303, 546-548, 1983

A:Title: Evidence on human origins from haemoglobins of African apes.

A:Reference number: A93303; MUID:83219265

A:Accession: D93303

A:Molecule type: protein

A:Residues: 1-146 <GOO>

C:Superfamily: globin; globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier

F:3-146/Domain: globin homology <GLB>

F:1-2,82,143/Binding site: 2,3-diphosphoglycerate (Val, His, Lys, His) #status predicted

F:62/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10
|||||
Db 32 LVVYPTQRF 41

RESULT 26

HBC2P

hemoglobin beta chain - common gibbon (tentative sequence)

C:Species: Hylobates lar (common gibbon, white-handed gibbon)
C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 03-Mar-2000
C:Accession: A02353
R:Boyer, S.H.; Crosby, E.F.; Noyes, A.N.; Fuller, G.F.; Leslie, S.E.; Donaldson, L.J.;
Biochem. Genet. 5, 405-448, 1971
A:Title: Primate hemoglobins: some sequences and some proposals concerning the character
A:Reference number: A90233; MUID:72020149
A:Accession: A02353
A:Molecule type: protein
A:Residues: 1-146 <BOY>
C:Comment: A common allelic sequence has 80-Asp and 87-Lys, and an uncommon allelic sequ
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrie
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTFQRF 10
|||||
DB 32 LVVYPWTFQRF 41

RESULT 27
HBMOP
hemoglobin beta chain - hanuman langur
C:Species: Presbytis entellus (hanuman langur)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
C:Accession: B02250; A02354
R:Matsumi, G.; Maita, T.; Nakashima, Y.; Barnabas, J.; Ranjekar, P.K.; Gandhi, N.S.
Int. J. Pept. Protein Res. 5, 423-425, 1973
A:Title: The primary structures of the alpha and beta polypeptide chains of adult hemog
A:Reference number: A02250; MUID:74115166
A:Accession: B02250
A:Molecule type: protein
A:Residues: 1-146 <MAT>
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrie
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTFQRF 10
|||||
DB 32 LVVYPWTFQRF 41

RESULT 28
HBMQJ
hemoglobin beta chain - Japanese macaque
C:Species: Macaca fuscata fuscata (Japanese macaque)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
C:Accession: A04622; A02354
R:Matsumi, G.; Maita, T.; Ota, H.; Tachikawa, I.; Tanaka, Y.; Araya, A.; Nakashima, Y.
Int. J. Protein Res. 3, 53-55, 1971
A:Title: The primary structure of the beta polypeptide chain of adult hemoglobin of the
A:Reference number: A04622; MUID:72030553
A:Accession: A04622
A:Molecule type: protein
A:Residues: 1-146 <MAT>
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrie
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTFQRF 10
|||||
DB 32 LVVYPWTFQRF 41

RESULT 29
HBMOPM
hemoglobin beta chain - pig-tailed macaque
C:Species: Macaca nemestrina (pig-tailed macaque)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 03-Mar-2000
C:Accession: S10689; S04300
R:Nute, P.E.; Patarayas, H.A.
Am. J. Phys. Anthropol. 40, 75-82, 1974
A:Title: Amino acid compositions of the tryptic peptides comprising the beta-hemoglob
A:Reference number: S10689; MUID:7412665
A:Accession: S10689
A:Molecule type: protein
A:Residues: 1-146 <NUM>
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metallopro
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTFQRF 10
|||||
DB 32 LVVYPWTFQRF 41

RESULT 30
HBMOC
hemoglobin beta chain - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
C:Accession: A29665; A04623; A02354
R:Savallier, P.; Trabuchet, G.; Chebloune, Y.; Faure, C.; Verdier, G.; Nigou, V.M.
J. Mol. Evol. 24, 309-318, 1987
A:Title: Nucleotide sequence of the beta-globin genes in gorilla and macaque: the ori
A:Reference number: A29665; MUID:87254238
A:Accession: A29665
A:Molecule type: DNA
A:Status: translation not shown
A:Residues: 1-120 <SAV>
A:Cross-references: EMBL:X05665; NID:g38042; PIDN:CAA29153.1; PID:g1333691
A:Experimental source: species designated as Macaca cynomolgus
A>Note: Initiator Met not translated
R:Wade, P.T.; Barnicot, N.A.; Huehns, E.R.
Biochem. Biophys. Acta 221, 450-466, 1970
A:Title: Structural studies on the major and minor haemoglobin of the monkey Macaca-1
A:Reference number: A04623; MUID:71108403
A:Accession: A04623
A:Molecule type: protein
A:Residues: 1-146 <WAD>
C:Genetics:
A:Introns: 30/3; 104/3
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen car
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFORF 10
|||||
DB 32 LVVYPWTFORF 41

RESULT 31

HBMBK
hemoglobin beta chain - green monkey
C:Species: Cercopithecus aethiops (green monkey, grivet)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
C:Accession: B02252; A02354
R:Matuda, G., Maita, T., Watanabe, B., Araya, A., Morokuma, K., Goodman, M., Prychodko, Hoppe-Seyler's Z. Physiol. Chem. 354, 1153-1155, 1973
A:Title: The amino acid sequences of the alpha and beta polypeptide chains of adult hemoglobin
A:Reference number: A02252; MUID:75040050
A:Accession: B02252
A:Molecule type: protein
A:Residues: 1-146 <MAT>
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFORF 10
|||||
DB 32 LVVYPWTFORF 41

RESULT 32

HBMBK
hemoglobin beta chain - mandrill
C:Species: Papio sphinx, Mandrillus sphinx (mandrill)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 03-Mar-2000
C:Accession: S00540
R:Lin, H.X.; Kleinschmidt, T.; Braunitzer, G.; Goeltenboth, R. Biol. Chem. Hoppe-Seyler 369, 209-216, 1988
A:Title: The primary structure of the mandrill (Mandrillus sphinx, primates) hemoglobin
A:Reference number: S00526; MUID:88293710
A:Accession: S00540
A:Molecule type: protein
A:Residues: 1-146 <LIN>
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFORF 10
|||||
DB 32 LVVYPWTFORF 41

RESULT 33

HBMBK
hemoglobin beta chain - gelada baboon
C:Species: Theropithecus gelada (gelada baboon)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000

C:Accession: A04620; A02354
R:Hewett-Emmett, D.; Barnicoat, N.A.
Unpublished results, cited in Hewett-Emmett, D., Ph.D. thesis, University of London,
Fasman, G.D., ed., pp.441-460, Chemical Rubber Co., Cleveland, 1976
A:Reference number: A04620
A:Accession: A04620
A:Molecule type: protein
A:Residues: 1-146 <HEW>
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFORF 10
|||||
DB 32 LVVYPWTFORF 41

RESULT 34

HBMBK
hemoglobin beta chain - yellow baboon
C:Species: Papio cynocephalus, Papio hamadryas cynocephalus (yellow baboon)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
C:Accession: A04624; A02354
R:Nute, P.E.; Mahoney, W.C. Hemoglobin 4, 109-123, 1980
A:Title: Complete primary structure of the beta chain from the hemoglobin of a baboon
A:Reference number: A04624; MUID:80227364
A:Accession: A04624
A:Molecule type: protein
A:Residues: 1-146 <NUT>
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFORF 10
|||||
DB 32 LVVYPWTFORF 41

RESULT 35

HBMBK
hemoglobin beta chain - red-crowned mangabey
C:Species: Cercocebus torquatus (red-crowned mangabey, white-collared mangabey)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
C:Accession: A04621; A02354
R:Cook, C.N.; Barnicoat, N.A. unpublished results, cited in Hewett-Emmett, D., Ph.D. thesis, University of London,
Fasman, G.D., ed., pp.441-460, Chemical Rubber Co., Cleveland, 1976
A:Reference number: A04621
A:Accession: A04621
A:Molecule type: protein
A:Residues: 1-146 <COO>
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORF 10
 |||||
 DB 32 LVVYPWTORF 41

RESULT 36

HBMQB
 hemoglobin beta chain - red colobus

C:Species: Colobus badius (red colobus)

C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000

C:Accession: B04620; A02354

R:Hewitt-Emmett, D.; Barnicot, N.A.

unpublished results, cited in Hewitt-Emmett, D., Ph.D. thesis, University of London, 197

F:63/Binding site: oxygen (His) (proximal axial ligand) #status predicted

F:92/Binding site: heme iron (His)

A:Reference number: A04620

A:Accession: B04620

A:Molecule type: protein

A:Residues: 1-146 <HEW>

C:Superfamily: globin; globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier

F:3-146/Domain: globin homology <GLB>

F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORF 10
 |||||
 DB 32 LVVYPWTORF 41

RESULT 37

HBMQB
 hemoglobin beta chain - brown-headed tamarin

C:Species: Saguinus fuscicollis (brown-headed tamarin, saddle-backed tamarin)

C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 03-Mar-2000

C:Accession: A02360

R:Lin, K.D.; Kim, Y.K.; Chernoff, A.I.

Biochem. Genet. 14, 427-440, 1976

A:Title: Primary structure of the marmoset (Saguinus fuscicollis) hemoglobin. I. Use of

A:Reference number: A90230; MUID:77021459

A:Accession: A02360

A:Molecule type: protein

A:Residues: 1-146 <LIN>

C:Superfamily: globin; globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier

F:3-146/Domain: globin homology <GLB>

F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORF 10
 |||||
 DB 32 LVVYPWTORF 41

RESULT 38

HBMQB
 hemoglobin beta chain - black-and-red tamarin (tentative sequence)

C:Species: Saguinus nigricollis (black-and-red tamarin)

C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 03-Mar-2000

C:Accession: A02358

R:Boyer, S.H.; Crosby, E.F.; Noyes, A.N.; Fuller, G.F.; Leslie, S.E.; Donaldson, L.J.
 Biochem. Genet. 5, 405-448, 1971

A:Title: Primate hemoglobins: some sequences and some proposals concerning the charac

A:Reference number: A90233; MUID:77020149

A:Accession: A02358

A:Molecule type: protein

A:Residues: 1-146 <BOY>

C:Superfamily: globin; globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier

F:3-146/Domain: globin homology <GLB>

F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORF 10
 |||||
 DB 32 LVVYPWTORF 41

RESULT 39

HBMKM
 hemoglobin beta chain - mustached tamarin (tentative sequence)

C:Species: Saguinus mystax (mustached tamarin)

C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 03-Mar-2000

C:Accession: A02359

R:Boyer, S.H.; Crosby, E.F.; Noyes, A.N.; Fuller, G.F.; Leslie, S.E.; Donaldson, L.J.

Biochem. Genet. 5, 405-448, 1971

A:Title: Primate hemoglobins: some sequences and some proposals concerning the charac

A:Reference number: A90233; MUID:77020149

A:Accession: A02359

A:Molecule type: protein

A:Residues: 1-146 <BOY>

C:Superfamily: globin; globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier

F:3-146/Domain: globin homology <GLB>

F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORF 10
 |||||
 DB 32 LVVYPWTORF 41

RESULT 40

HBCRB
 hemoglobin beta chain - black-tailed marmoset

C:Species: Callithrix argentata (black-tailed marmoset)

C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000

C:Accession: S06513

R:Malta, T.; Hayashida, M.; Matsuda, G.

J. Biochem. 95, 805-813, 1984

A:Title: Primary structures of adult hemoglobins of silvery marmoset, Callithrix arge

A:Reference number: S06512; MUID:84212383

A:Accession: S06513

A:Molecule type: protein

A:Residues: 1-146 <MAI>

C:Superfamily: globin; globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metallopro

F:3-146/Domain: globin homology <GLB>

F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPMWTF 10
Db 32 LVVYPMWTF 41

RESULT 41

HBMQA

hemoglobin beta chain - white-fronted capuchin

C:Species: Cebus albifrons (white-fronted capuchin, pale-fronted capuchin)

C>Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 11-May-2000

C:Accession: A02361

R:Nute, P.E.; Sullivan, B.

Comp. Biochem. Physiol. B 39, 797-814, 1971

A:Title: Primate hemoglobins: their structure, function and evolution. I. Amino acid com

A:Reference number: A02361; MUID:72076589

A:Accession: A02361

A:Molecule type: protein

A:Residues: 1-146 <NUT>

A:Note: 13-Thr was found in half of the beta chains from one monkey

C:Superfamily: globin; globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier

F:3-146/Domain: globin homology <GLB>

F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPMWTF 10
Db 32 LVVYPMWTF 41

RESULT 42

HBMQA

hemoglobin beta chain - brown capuchin

C:Species: Cebus apella (brown capuchin, black-capped capuchin)

C>Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 03-Mar-2000

C:Accession: A02362

R:Matanabe, B.

Selragaku 46, 255-267, 1974

A:Title: Amino acid sequences of the tryptic peptides from the beta chain of hemoglobin

A:Reference number: A02362; MUID:75042140

A:Accession: A02362

A:Molecule type: protein

A:Residues: 1-146 <MAT>

C:Superfamily: globin; globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier

F:3-146/Domain: globin homology <GLB>

F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPMWTF 10
Db 32 LVVYPMWTF 41

RESULT 43

HBMKN

hemoglobin beta chain - douroucouli (tentative sequence)

C:Species: Aotus trivirgatus (douroucouli, night monkey, owl monkey)

C>Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 03-Mar-2000

C:Accession: A02356

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

R:Boyer, S.H.; Crosby, E.F.; Noyes, A.N.; Fuller, G.F.; Leslie, S.E.; Donaldson, L.J.
Biochem. Genet. 5, 405-448, 1971

A:Title: Primate hemoglobins: some sequences and some proposals concerning the charac
A:Reference number: A90233; MUID:72020149

A:Accession: A02356

A:Molecule type: protein

A:Residues: 1-146 <BOY>

C:Superfamily: globin; globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen car

F:3-146/Domain: globin homology <GLB>

F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00017;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPMWTF 10
Db 32 LVVYPMWTF 41

RESULT 44

HBMKP

hemoglobin beta chain - black-handed spider monkey

C:Species: Ateles geoffroyi (black-handed spider monkey)

C>Date: 24-Apr-1984 #sequence_revision 28-May-1986 #text_change 03-Mar-2000

C:Accession: A90233; A02355

R:Boyer, S.H.; Crosby, E.F.; Noyes, A.N.; Fuller, G.F.; Leslie, S.E.; Donaldson, L.J.

Biochem. Genet. 5, 405-448, 1971

A:Title: Primate hemoglobins: some sequences and some proposals concerning the charac

A:Reference number: A90233; MUID:72020149

A:Accession: A90233

A:Molecule type: protein

A:Residues: 1-146 <BOY>

C:Superfamily: globin; globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen car

F:3-146/Domain: globin homology <GLB>

F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00017;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPMWTF 10
Db 32 LVVYPMWTF 41

RESULT 45

HBMKH

hemoglobin beta chain - long-haired spider monkey

C:Species: Ateles belzebuth (long-haired spider monkey)

C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 03-Mar-2000

C:Accession: B90233; A02355

R:Boyer, S.H.; Crosby, E.F.; Noyes, A.N.; Fuller, G.F.; Leslie, S.E.; Donaldson, L.J.

Biochem. Genet. 5, 405-448, 1971

A:Title: Primate hemoglobins: some sequences and some proposals concerning the charac

A:Reference number: A90233; MUID:72020149

A:Accession: B90233

A:Molecule type: protein

A:Residues: 1-146 <BOY>

C:Superfamily: globin; globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen car

F:3-146/Domain: globin homology <GLB>

F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
|||||
Db 32 LVVYPWTORE 41

RESULT 46

HBMKK

hemoglobin beta chain - black spider monkey

C:Species: Ateles paniscus (black spider monkey)

C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 03-Mar-2000

C:Accession: A90034; A02355

R:Boyer, S.H.; Crosby, E.F.; Fuller, G.F.; Noyes, A.N.; Adams, J.G.

Ann. N. Y. Acad. Sci. 165, 360-377, 1969

A:Title: The structure and biosynthesis of hemoglobins A and A-2 in the new world primate

A:Reference number: A90034; MUID:70031568

A:Accession: A90034

A:Molecule type: protein

A:Residues: 1-146 <BOY>

C:Superfamily: globin; globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier

F:3-146/Domain: globin homology <GLB>

F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
|||||
Db 32 LVVYPWTORE 41

RESULT 47

HBMKS

hemoglobin beta chain - common squirrel monkey (tentative sequence)

C:Species: Saimiri sciureus (common squirrel monkey)

C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 03-Mar-2000

C:Accession: A02357

R:Boyer, S.H.; Crosby, E.F.; Noyes, A.N.; Fuller, G.F.; Leslie, S.E.; Donaldson, L.J.; V

Biochem. Genet. 5, 405-448, 1971

A:Title: Primate hemoglobins: some sequences and some proposals concerning the character

A:Reference number: A90233; MUID:72020149

A:Accession: A02357

A:Molecule type: protein

A:Residues: 1-146 <BOY>

A>Note: an allelic sequence has 76-Thr

C:Superfamily: globin; globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier

F:3-146/Domain: globin homology <GLB>

F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
|||||
Db 32 LVVYPWTORE 41

RESULT 48

HBMKA

hemoglobin beta chain - Amazon manatee

C:Species: Trichechus inunguis (Amazon manatee, Brazilian manatee)

C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 03-Mar-2000

C:Accession: S00821; B24929

R:Kleinschmidt, T.; Braunitzer, G.; Best, R.
Biol. Chem. Hoppe-Seyler 369, 507-512, 1988

A:Title: The primary structure of the hemoglobin of the Brazilian manatee (Trichechus

A:Reference number: S00820; MUID:89076485

A:Accession: S00821

A:Molecule type: protein

A:Residues: 1-146 <KL>

R:Kleinschmidt, T.; Czelusniak, J.; Goodman, M.; Braunitzer, G.

Mol. Biol. Evol. 3, 427-435, 1986

A:Title: Paenungulata: a comparison of the hemoglobin sequences from elephant, hyrax,

A:Reference number: A93060; MUID:88174362

A:Accession: B24929

A:Molecule type: protein

A:Residues: 1-146 <KL2>

C:Superfamily: globin; globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metallopro

F:3-146/Domain: globin homology <GLB>

F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
|||||
Db 32 LVVYPWTORE 41

RESULT 49

HBDHU

hemoglobin delta chain - human

C:Species: Homo sapiens (man)

C:Date: 30-Apr-1980 #sequence_revision 30-Apr-1980 #text_change 03-Mar-2000

C:Accession: A90804; A91678; A02363

R:Spitz, R.A.; Dertiel, J.K.; Forget, B.G.; Weissman, S.M.

Cell 21, 639-646, 1980

A:Title: Complete nucleotide sequence of the human delta-globin gene.

A:Reference number: A90804; MUID:81064666

A:Accession: A90804

A:Molecule type: DNA

A:Residues: 1-146 <SPR>

A:Cross-references: GB:V00505; NID:930510; PTDN:CAA23763.1; PID:930511

R:Brannitz, G.; Schrank, B.; Stangl, A.; Grillemeier, M.

Hoppe-Seyler's Z. Physiol. Chem. 359, 777-783, 1978

A:Title: Notiz zur Sequenz der delta Ketten der menschlichen Haemoglobine (Hb A-2 - a

A:Reference number: A91678; MUID:78240319

A:Accession: A91678

A:Molecule type: protein

A:Residues: 1-146

C:Genetics:

A:Gene: GDB:HB

A:Cross-references: GDB:119298; OMIM:142000

A:Map position: 11p15.5-11p15.5

C:Function: two delta chains combine in heterotetramers with two alpha chains (see PIR

C:Description: in erythrocytes binds and transports molecular oxygen from lung to tis

C:Superfamily: globin; globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metallopro

F:3-146/Domain: globin homology <GLB>

F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
|||||
Db 32 LVVYPWTORE 41

RESULT 50
HDCZ
hemoglobin delta chain - chimpanzee (tentative sequence)
C:Species: Pan troglodytes (chimpanzee)
C:Date: 28-Feb-1986 #sequence_revision 28-Feb-1986 #text_change 03-Mar-2000
C:Accession: C90233; A93402; A02364
R:Boyer, S.H.; Crosby, E.F.; Noyes, A.N.; Fuller, G.F.; Leslie, S.E.; Donaldson, L.J.; V
Biochem. Genet. 5, 405-448, 1971
A:Title: Primate hemoglobins: some sequences and some proposals concerning the character
A:Reference number: A90233; MUID:72020149
A:Accession: C90233
A:Molecule type: protein
A:Residues: 1-146 <BOY>
R:de Jong, W.M.W.
Nature New Biol. 234, 176-177, 1971
A:Title: Structure of the delta-chain of chimpanzee haemoglobin A-2.
A:Reference number: A93402; MUID:72089100
A:Accession: A93402
A:Molecule type: protein
A:Residues: 1-146 <DEJ>
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LVVYPWTFORF 10
DB 32 LVVYPWTFORF 41

RESULT 51
HDCO
hemoglobin delta chain - gorilla (tentative sequence)
C:Species: Gorilla gorilla (gorilla)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 03-Mar-2000
C:Accession: D90233; A02364
R:Boyer, S.H.; Crosby, E.F.; Noyes, A.N.; Fuller, G.F.; Leslie, S.E.; Donaldson, L.J.; V
Biochem. Genet. 5, 405-448, 1971
A:Title: Primate hemoglobins: some sequences and some proposals concerning the character
A:Reference number: A90233; MUID:72020149
A:Accession: D90233
A:Molecule type: protein
A:Residues: 1-146 <BOY>
A:Note: an allele of the gorilla sequence has 126-Ala
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LVVYPWTFORF 10
DB 32 LVVYPWTFORF 41

RESULT 52
HDCI
hemoglobin delta chain - gibbon (tentative sequence)
C:Species: Hylobates sp. (gibbon)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 03-Mar-2000
C:Accession: E90233; A02364

R:Boyer, S.H.; Crosby, E.F.; Noyes, A.N.; Fuller, G.F.; Leslie, S.E.; Donaldson, L.J.
Biochem. Genet. 5, 405-448, 1971
A:Title: Primate hemoglobins: some sequences and some proposals concerning the charac
A:Reference number: A90233; MUID:72020149
A:Accession: E90233
A:Molecule type: protein
A:Residues: 1-146 <BOY>
A:Note: a common allele of the gibbon sequence has 6- or 7-Gly
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen car
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LVVYPWTFORF 10
DB 32 LVVYPWTFORF 41

RESULT 53
HDMKP
hemoglobin delta chain - black-handed spider monkey
C:Species: Ateles geoffroyi (black-handed spider monkey)
C:Date: 24-Apr-1984 #sequence_revision 30-Sep-1993 #text_change 03-Mar-2000
C:Accession: A31523; B02365; A02365
R:Spitz, R.A.; Giebel, L.B.
Mol. Biol. Evol. 5, 21-29, 1988
A:Title: The structure and evolution of the spider monkey delta-globin gene.
A:Reference number: A31523; MUID:88189005
A:Accession: A31523
A:Molecule type: DNA
A:Residues: 1-146 <SPR>
A:Cross-references: GB:M19061; NID:g342379; PIDN:AA00793.1; PID:g342380
A:Note: the authors translated the codon AAG for residue 132 as Glu

R:Boyer, S.H.; Crosby, E.F.; Noyes, A.N.; Fuller, G.F.; Leslie, S.E.; Donaldson, L.J.
Biochem. Genet. 5, 405-448, 1971
A:Title: Primate hemoglobins: some sequences and some proposals concerning the charac
A:Reference number: A90233; MUID:72020149
A:Accession: B02365
A:Molecule type: protein
A:Residues: 1-146, 'G', '6-8', 'S', '10-46', 'A', '48-51', 'D', '53-146' <BOY>
A:Note: three alleles of the sequence shown have 6-Lys, 9-Ala, and 69-Asp, respective
C:Genetics:
A:Introns: 30/2; 104/3
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen car
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LVVYPWTFORF 10
DB 32 LVVYPWTFORF 41

RESULT 54
HDMKH
hemoglobin delta chain - brown-headed spider monkey (tentative sequence)
C:Species: Ateles fusciceps (brown-headed spider monkey)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 03-Mar-2000
C:Accession: C02365; A02365
R:Boyer, S.H.; Crosby, E.F.; Noyes, A.N.; Fuller, G.F.; Leslie, S.E.; Donaldson, L.J.
Biochem. Genet. 5, 405-448, 1971

A:Title: Primate hemoglobins: some sequences and some proposals concerning the character
A:Reference number: A90233; MUID:72020149
A:Accession: G02365
A:Molecule type: protein
A:Residues: 1-146 <BOY>
A:Note: three alleles of the sequence shown have 6-Lys, 9-Ala, and 69-Asp, respectively
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
|||||
Db 32 LVVYPWTQRF 41

RESULT 55

HDMKTM hemoglobin delta chain - moustached tamarin (tentative sequence)

C:Species: Saguinus mystax (moustached tamarin)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 03-Mar-2000
C:Accession: D02365; A02365
R:Boyer, S.H.; Crosby, E.F.; Noyes, A.N.; Fuller, G.F.; Leslie, S.E.; Donaldson, L.J.;
Biochem. Genet. 5, 405-448, 1971
A:Title: Primate hemoglobins: some sequences and some proposals concerning the character
A:Reference number: A90233; MUID:72020149
A:Accession: D02365
A:Molecule type: protein
A:Residues: 1-146 <BOY>
A:Note: residues 16 and 12 may be Gly and Ser, respectively
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
|||||
Db 32 LVVYPWTQRF 41

RESULT 56

HDMKTB hemoglobin delta chain - black-and-red tamarin (tentative sequence)

C:Species: Saguinus nigricollis (black-and-red tamarin)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 03-Mar-2000
C:Accession: E02365; A02365
R:Boyer, S.H.; Crosby, E.F.; Noyes, A.N.; Fuller, G.F.; Leslie, S.E.; Donaldson, L.J.;
Biochem. Genet. 5, 405-448, 1971
A:Title: Primate hemoglobins: some sequences and some proposals concerning the character
A:Reference number: A90233; MUID:72020149
A:Accession: E02365
A:Molecule type: protein
A:Residues: 1-146 <BOY>
A:Note: residues 16 and 12 may be Gly and Ser, respectively
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
|||||
Db 32 LVVYPWTQRF 41

RESULT 57

HDMKDU

hemoglobin delta chain - douroucouli (tentative sequence)

C:Species: Aotus trivirgatus (douroucouli, night monkey, owl monkey)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 03-Mar-2000
C:Accession: F02365; A02365
R:Boyer, S.H.; Crosby, E.F.; Noyes, A.N.; Fuller, G.F.; Leslie, S.E.; Donaldson, L.J.;
Biochem. Genet. 5, 405-448, 1971
A:Title: Primate hemoglobins: some sequences and some proposals concerning the charac
A:Reference number: A90233; MUID:72020149
A:Accession: F02365
A:Molecule type: protein
A:Residues: 1-146 <BOY>
A:Note: residue 125 may be Gln and residue 127 or 131 may be Leu
A:Note: an allelic sequence has 120-Asn
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen car
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
|||||
Db 32 LVVYPWTQRF 41

RESULT 58

HDMKSO

hemoglobin delta chain - common squirrel monkey (tentative sequence)

C:Species: Saimiri sciureus (common squirrel monkey)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 03-Mar-2000
C:Accession: G02365; A02365
R:Boyer, S.H.; Crosby, E.F.; Noyes, A.N.; Fuller, G.F.; Leslie, S.E.; Donaldson, L.J.;
Biochem. Genet. 5, 405-448, 1971
A:Title: Primate hemoglobins: some sequences and some proposals concerning the charac
A:Reference number: A90233; MUID:72020149
A:Accession: G02365
A:Molecule type: protein
A:Residues: 1-146 <BOY>
A:Note: residues 16 and 12 may be Gly and Ser, respectively. Residues 51 and 58 may b
A:Note: an allelic sequence has 121-Gln
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen car
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
|||||
Db 32 LVVYPWTQRF 41

RESULT 59

HBLRSL

hemoglobin beta chain - slow loris
C:Species: Nycticebus coucang (slow loris)
C:Date: 24-Apr-1984 #sequence_revision 31-Dec-1991 #text_change 03-Mar-2000
C:Accession: A02366
R:Matsumoto, G.; Matsuda, T.; Matsumoto, B.; Ota, H.; Araya, A.; Goodman, M.; Prychodko, W.
Int. J. Pept. Protein Res. 5, 419-421, 1973
A:Title: The primary structures of the alpha and beta polypeptide chains of adult hemog
A:Reference number: A91767; MUID:74115165
A:Accession: A02366
A:Molecule type: protein
A:Residues: 1-146 <MAT>
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprote
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVYPWTFQRF 10
|||||
Db 32 LVVYPWTFQRF 41

RESULT 60
HBLRN
hemoglobin beta chain - slender loris
C:Species: Loris tardigradus (slender loris)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 03-Mar-2000
C:Accession: B91949
R:Matsumoto, T.; Goodman, M.; Matsuda, G.
J. Biochem. 84, 377-383, 1978
A:Title: Amino acid sequences of the alpha and beta chains of adult hemoglobin of the sl
A:Reference number: A91949; MUID:79027141
A:Accession: B91949
A:Molecule type: protein
A:Residues: 1-146 <MAT>
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprote
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVYPWTFQRF 10
|||||
Db 32 LVVYPWTFQRF 41

RESULT 61
HBGC
hemoglobin beta-I chain - thick-tailed bush baby
C:Species: Galago crassicaudatus, Otollemur crassicaudatus (thick-tailed bush baby)
C:Date: 28-Aug-1985 #sequence_revision 31-Dec-1991 #text_change 03-Mar-2000
C:Accession: A02367
R:Matsumoto, B.; Fujii, T.; Nakashima, Y.; Matsuda, T.; Matsuda, G.
Biol. Chem. Hoppe-Seyler 366, 265-269, 1985
A:Title: Amino-acid sequences of the alpha and beta chains of adult hemoglobins of the g
A:Reference number: A90683; MUID:85225956
A:Accession: A02367
A:Molecule type: protein
A:Residues: 1-146 <MAT>
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprote
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVYPWTFQRF 10
|||||
Db 32 LVVYPWTFQRF 41

RESULT 62
HBGC2
hemoglobin beta-II chain - thick-tailed bush baby
C:Species: Galago crassicaudatus, Otollemur crassicaudatus (thick-tailed bush baby)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 03-Mar-2000
C:Accession: A90683
R:Matsumoto, B.; Fujii, T.; Nakashima, Y.; Matsuda, T.; Matsuda, G.
Biol. Chem. Hoppe-Seyler 366, 265-269, 1985
A:Title: Amino-acid sequences of the alpha and beta chains of adult hemoglobins of th
A:Reference number: A90683; MUID:85225956
A:Accession: A90683
A:Molecule type: protein
A:Residues: 1-146 <MAT>
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metallopro
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVYPWTFQRF 10
|||||
Db 32 LVVYPWTFQRF 41

RESULT 63
HBTB
hemoglobin beta chain - western tarsier (tentative sequence)
C:Species: Tarsius bancanus (western tarsier)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C:Accession: A02368
R:Beard, J.M.; Barnicot, N.A.; Hewett-Emmett, D.
Nature 259, 338-341, 1976
A:Title: Alpha and beta chains of the major haemoglobin and a note on the minor compo
A:Reference number: A93178; MUID:76126211
A:Accession: A02368
A:Molecule type: protein
A:Residues: 1-146 <BEA>
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen car
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVYPWTFQRF 10
|||||
Db 32 LVVYPWTFQRF 41

RESULT 64
HBLER
hemoglobin beta chain - brown lemur (tentative sequence)

C:Species: Lemur fulvus fulvus (brown lemur)
C:Date: 30-Sep-1979 #sequence_revision 30-Sep-1979 #text_change 31-Mar-2000
C:Accession: A02370
R:Matita, T.; Setoguchi, M.; Matsuda, G.; Goodman, M.
J. Biochem. 85, 755-764, 1979
A:Title: Amino acid sequences of the alpha and beta chains of adult hemoglobin of the br
A:Reference number: A91952; MUID:79150872
A:Accession: A02370
A:Molecule type: protein
A:Residues: 1-146 <MAT>
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
|||||
Db 32 LVVYPWTORE 41

RESULT 65
HBBEC
hemoglobin beta chain - ring-tailed lemur
C:Species: Lemur catta (ring-tailed lemur)
C:Date: 18-Aug-1982 #sequence_revision 17-Mar-1987 #text_change 03-Mar-2000
C:Accession: A02371
R:Copenhaver, D.H.; Dixon, J.D.; Duffy, L.K.
Hemoglobin 7, 1-14, 1983
A:Title: Proximal hemoglobins I. The primary structure of the beta-globin chain of Lemu
A:Reference number: A02371; MUID:83185437
A:Accession: A02371
A:Molecule type: protein
A:Residues: 1-146 <COR>
A:Note: residues 125-131 were positioned by homology
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
|||||
Db 32 LVVYPWTORE 41

RESULT 66
S06511
hemoglobin beta chain - ruffed lemur
C:Species: Varecia variegata (ruffed lemur)
C:Date: 30-Sep-1991 #sequence_revision 03-Oct-1995 #text_change 03-Mar-2000
C:Accession: S06511
R:Duffy, L.K.; Copenhaver, D.H.
In Brussels hemoglobin symposium, Schneck, A.G., and Paul, C., eds., pp. 377-392, Edition
A:Title: Proximal hemoglobins II. Comparison of hemoglobin beta-chain primary structure
A:Reference number: S06511
A:Accession: S06511
A:Molecule type: protein
A:Residues: 1-146 <DUF>
A:Note: The source is designated as Lemur variegatus
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F:3-146/Domain: globin homology <GLB>

F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
|||||
Db 32 LVVYPWTORE 41

RESULT 67
HBBRTG
hemoglobin beta chain - northern gundi
C:Species: Ctenodactylus gundi (northern gundi)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 03-Mar-2000
C:Accession: S13283; C33082
R:Beintema, J.J.; Rodewald, K.; Braunltzer, G.
Biol. Chem. Hoppe-Seyler 371, 1089-1093, 1990
A:Title: The primary structures of gundi (Ctenodactylus gundi, Rodentia) hemoglobin a
A:Reference number: S13282; MUID:91197427
A:Accession: S13283
A:Molecule type: protein
A:Residues: 1-146 <BEI>
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metallopro
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
|||||
Db 32 LVVYPWTORE 41

RESULT 68
HBBRT
hemoglobin beta chain - raccoon
C:Species: Procyon lotor (raccoon)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
C:Accession: S06525
R:Brimhall, B.; Stangland, K.; Jones, R.T.; Becker, R.R.; Bailey, T.J.
Hemoglobin 2, 351-370, 1978
A:Title: Amino acid sequence of the hemoglobin of raccoon (Procyon lotor).
A:Reference number: S06524; MUID:79026831
A:Accession: S06525
A:Molecule type: protein
A:Residues: 1-146 <BRI>
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metallopro
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
|||||
Db 32 LVVYPWTORE 41

RESULT 69
HBBRT

hemoglobin beta chain - Asiatic black bear
C:Species: Ursus tibetanus (Asiatic black bear)
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 03-Mar-2000
C:Accession: A90709
R:Hofmann, O.; Schreitmüller, T.; Braunitzer, G.; Wiesner, M.V.H.
Biol. Chem. Hoppe-Seyler 367, 53-59, 1986
A:Title: The primary structure of polar bear (Ursus maritimus, Carnivora) and Asiatic black bear (Ursus tibetanus, Carnivora) hemoglobin beta chains
A:Reference number: A90709; MUID:86159301
A:Accession: A90709
A:Molecule type: protein
A:Residues: 1-146 <HOF>
A>Note: article in German with English abstract
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTO RF 10
|||||
DB 32 LVVYPWTO RF 41

RESULT 70

HBHBM
hemoglobin beta chain - polar bear
C:Species: Ursus maritimus (polar bear)
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 03-Mar-2000
C:Accession: B25880
R:Hofmann, O.; Schreitmüller, T.; Braunitzer, G.; Wiesner, M.V.H.
Biol. Chem. Hoppe-Seyler 367, 53-59, 1986
A:Title: The primary structure of polar bear (Ursus maritimus, Carnivora) and Asiatic black bear (Ursus tibetanus, Carnivora) hemoglobin beta chains
A:Reference number: A90709; MUID:86159301
A:Accession: B25880
A:Molecule type: protein
A:Residues: 1-146 <HOF>
A>Note: article in German with English abstract
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTO RF 10
|||||
DB 32 LVVYPWTO RF 41

RESULT 71

HBFOU
hemoglobin beta chain - lesser panda
C:Species: Allurus fulgens (lesser panda)
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
C:Accession: S06527
R:Tagle, D.A.; Miyamoto, M.M.; Goodman, M.; Hofmann, O.; Braunitzer, G.; Goeltenboth, R.
Naturwissenschaften 73, 512-514, 1986
A:Title: Hemoglobin of pandas: phylogenetic relationships of carnivores as ascertained by molecular cloning
A:Reference number: S06526; MUID:87014854
A:Accession: S06527
A:Molecule type: protein
A:Residues: 1-146 <TAG>
A>Note: article in German with English abstract
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTO RF 10
|||||
DB 32 LVVYPWTO RF 41

RESULT 72

HBFOG
hemoglobin beta chain - giant panda
C:Species: Alluropoda melanoleuca (giant panda)
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
C:Accession: S06529
R:Tagle, D.A.; Miyamoto, M.M.; Goodman, M.; Hofmann, O.; Braunitzer, G.; Goeltenboth, R.
Naturwissenschaften 73, 512-514, 1986
A:Title: Hemoglobin of pandas: phylogenetic relationships of carnivores as ascertained by molecular cloning
A:Reference number: S06526; MUID:87014854
A:Accession: S06529
A:Molecule type: protein
A:Residues: 1-146 <TAG>
A>Note: article in German with English abstract
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTO RF 10
|||||
DB 32 LVVYPWTO RF 41

RESULT 73

HBHM
hemoglobin beta chain - domestic ferret
C:Species: Mustela putorius furo (domestic ferret)
C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 03-Mar-2000
C:Accession: S11534
R:Pauplin, Y.; Hombrados, I.; Faure, F.; Han, K.K.; Neuzil, E.
Biochem. Soc. Trans. 16, 608-609, 1988
A:Title: The primary structure of the beta-chain of the haemoglobins of the ferret (Mustela putorius furo)
A:Reference number: S11534
A:Accession: S11534
A:Molecule type: protein
A:Residues: 1-146 <PAU>
A>Note: article in German with English abstract
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTO RF 10
|||||
DB 32 LVVYPWTO RF 41

RESULT 74

HBOTE

hemoglobin beta chain - Eurasian river otter

C:Species: Lutra lutra (Eurasian river otter)

C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 03-Mar-2000

C:Accession: S00817

R:Lin, H.X.; Kleinschmidt, T.; Braunitzer, G.; Schell, H.G.

Biol. Chem. Hoppe-Seyler 369, 349-355, 1988

A:Title: Carnivora: the primary structure of the common otter (Lutra lutra, Mustelidae)

A:Reference number: S00816; MUID:89000194

A:Accession: S00817

A:Molecule type: protein

A:Residues: 1-146 <LIN>

C:Superfamily: globin: globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein

F:3-146/Domain: globin homology <GLB>

F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match

100.0%; Score 10; DB 1; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00017;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTORF 10

DB 32 LVVYPWTORF 41

RESULT 75

HBOTG

hemoglobin beta chain - giant otter

C:Species: Pteronura brasiliensis (giant otter)

C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000

C:Accession: S02081

R:Kleinschmidt, T.; Braunitzer, G.; Schell, H.G.

Biol. Chem. Hoppe-Seyler 370, 35-40, 1989

A:Title: Carnivora: the primary structure of the giant otter (Pteronura brasiliensis, M

A:Reference number: S02080; MUID:89228546

A:Accession: S02081

A:Molecule type: protein

A:Residues: 1-146 <KLE>

C:Superfamily: globin: globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein

F:3-146/Domain: globin homology <GLB>

F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match

100.0%; Score 10; DB 1; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00017;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTORF 10

DB 32 LVVYPWTORF 41

RESULT 76

HBMNE

hemoglobin beta chain - European mink

C:Species: Mustela lutreola (European mink)

C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-May-2000

C:Accession: S10105

R:Ahmed, A.; Jahan, M.; Braunitzer, G.

Z. Naturforsch. C 45, 223-228, 1990

A:Title: Carnivora: the amino acid sequence of the adult European mink (Mustela lutreola

A:Reference number: S10104; MUID:90303485

A:Accession: S10105

A:Molecule type: protein

A:Residues: 1-146 <AHM>

C:Superfamily: globin: globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein

F:3-146/Domain: globin homology <GLB>

F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match

100.0%; Score 10; DB 1; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00017;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTORF 10

DB 32 LVVYPWTORF 41

RESULT 77

HBOKE

hemoglobin beta chain - European polecat

C:Species: Mustela putorius (European polecat)

C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 03-Mar-2000

C:Accession: S10103

R:Ahmed, A.; Jahan, M.; Braunitzer, G.; Pechlaner, H.

Z. Naturforsch. B 44, 817-824, 1989

A:Title: Carnivora: the amino acid sequence of the adult European polecat (Mustela pu

A:Reference number: S10102

A:Accession: S10103

A:Molecule type: protein

A:Residues: 1-146 <AHM>

C:Superfamily: globin: globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein

F:3-146/Domain: globin homology <GLB>

F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match

100.0%; Score 10; DB 1; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00017;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTORF 10

DB 32 LVVYPWTORF 41

RESULT 78

HBBDR

hemoglobin beta chain - ratel

C:Species: Mellivora capensis (ratel)

C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000

C:Accession: S01663

R:Rodewald, K.; Braunitzer, G.; Goeltenboth, R.

Biol. Chem. Hoppe-Seyler 369, 1137-1142, 1988

A:Title: Carnivora: the primary structure of the hemoglobins from ratel (Mellivora capens

A:Reference number: S01662; MUID:89207098

A:Accession: S01663

A:Molecule type: protein

A:Residues: 1-146 <ROD>

C:Superfamily: globin: globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein

F:3-146/Domain: globin homology <GLB>

F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match

100.0%; Score 10; DB 1; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00017;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTORF 10

DB 32 LVVYPWTORF 41

RESULT 79

HBBDM

hemoglobin beta chain - beech marten
C:Species: Martes foina (beech marten)
C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 03-Mar-2000
C:Accession: S10599
R:Ruecknagel, K.P.; Miesner, H.; Braunitzer, G.
Biol. Chem. Hoppe-Seyler 371, 503-509, 1990
A:Title: Carnivora: the primary structure of the beech marten (Martes foina, Mustelidae)
A:Reference number: S10598; MUID:90359058
A:Accession: S10599
A:Molecule type: protein
A:Residues: 1-146 <BIO>
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFQRF 10
|||
Db 32 LVVYPWTFQRF 41

RESULT 80
HBHM
hemoglobin beta chain - Pacific walrus
C:Species: Odobenus rosmarus divergens (Pacific walrus)
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
C:Accession: S02820
R:Lin, H.X.; Kleinschmidt, T.; Johnson, M.L.; Braunitzer, G.
Biol. Chem. Hoppe-Seyler 370, 135-140, 1989
A:Title: Carnivora: the primary structure of the Pacific walrus (Odobenus rosmarus divergens)
A:Reference number: S02819; MUID:89207123
A:Accession: S02820
A:Molecule type: protein
A:Residues: 1-146 <LIN>
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFQRF 10
|||
Db 32 LVVYPWTFQRF 41

RESULT 81
B61434
hemoglobin beta chain - Galapagos fur seal
C:Species: Arctocepalus galapagensis (Galapagos fur seal)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Mar-2000
C:Accession: B61434
R:Jahan, M.; Ahmed, A.; Trillmich, F.; Braunitzer, G.
J. Protein Chem. 10, 257-263, 1991
A:Title: The complete primary structure of the marine carnivora, Galapagos fur seal (Arctocepalus galapagensis)
A:Reference number: A61434; MUID:92000163
A:Accession: B61434
A:Molecule type: protein
A:Residues: 1-146 <JAH>
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFQRF 10
|||
Db 32 LVVYPWTFQRF 41

RESULT 82
HBSLM
hemoglobin beta chain - Weddell seal
C:Species: Leptonychotes weddellii (Weddell seal)
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
C:Accession: S04952
R:Lin, H.; Kleinschmidt, T.; Braunitzer, G.; Schell, H.G.
Biol. Chem. Hoppe-Seyler 370, 707-713, 1989
A:Title: Carnivora: the primary structure of Weddell seal (Leptonychotes weddellii, P1)
A:Reference number: S04951; MUID:89374816
A:Accession: S04952
A:Molecule type: protein
A:Residues: 1-146 <LIN>
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFQRF 10
|||
Db 32 LVVYPWTFQRF 41

RESULT 83
HBBD
hemoglobin beta chain - bottle-nosed dolphin
C:Species: Tursiops truncatus (bottle-nosed dolphin)
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
C:Accession: S06523
R:Kleinschmidt, T.; Braunitzer, G.
Biomed. Biochim. Acta 42, 685-695, 1983
A:Title: The primary structure of the bottlenosed dolphin (Tursiops truncatus, Cetace)
A:Reference number: S06522; MUID:84052510
A:Accession: S06523
A:Molecule type: protein
A:Residues: 1-146 <KLE>
A:Note: article in German with English abstract
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFQRF 10
|||
Db 32 LVVYPWTFQRF 41

RESULT 84
HBMRK

hemoglobin beta chain - minke whale
C:Species: Balanoptera acutorostrata (minke whale, lesser rorqual)
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
C:Accession: S06521
R:Abbasl, A.; Rucknagel, P.; Matsuda, G.; Zaidi, Z.H.; Braunitzer, G.
J. Chem. Soc. Pak. 6, 253-256, 1984
A:Title: The primary structure of Minke-whale (Balanoptera acutorostrata - Cetacea) hemoglobin
A:Reference number: S06520
A:Accession: S06521
A:Molecule type: protein
A:Residues: 1-146 <ABB>
A>Note: 72-Ala, 87-Ala, 123-Leu, and 128-Ser were also found
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFQRF 10
|||||
Db 32 LVVYPWTFQRF 41

RESULT 85
HBBTV
hemoglobin beta chain - false vampire bat (Megaderma lyra)
C:Species: Megaderma lyra
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
C:Accession: S00541
R:SGouras, J.G.; Kleinschmidt, T.; Braunitzer, G.
Biol. Chem. Hoppe-Seyler 369, 47-53, 1988
A:Title: The primary structure of the hemoglobin of the Indian false vampire (Megaderma
A:Reference number: S00524; MUID:88163088
A:Accession: S00541
A:Molecule type: protein
A:Residues: 1-146 <SGO>
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFQRF 10
|||||
Db 32 LVVYPWTFQRF 41

RESULT 86
HBBZS
hemoglobin beta chain - spotted hyena
C:Species: Crocuta crocuta (spotted hyena)
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
C:Accession: S04221
R:He, C.; Rodewald, K.; Braunitzer, G.; Goeltenboth, R.
Biol. Chem. Hoppe-Seyler 370, 417-423, 1989
A:Title: Carlihora: primary structure of the hemoglobin from the spotted hyena (Crocuta
A:Reference number: S04220; MUID:89302684
A:Accession: S04221
A:Molecule type: protein
A:Residues: 1-146 <HBC>
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein
F:3-146/Domain: globin homology <GLB>

F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFQRF 10
|||||
Db 32 LVVYPWTFQRF 41

RESULT 87
HBDP
hemoglobin beta chain - Amur leopard
C:Species: Panthera pardus orientalis (Amur leopard)
C>Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 03-Mar-2000
C:Accession: A02373
R:Abbasl, A.; Braunitzer, G.
J. Protein Chem. 4, 57-67, 1985
A:Title: The primary structure of haemoglobin from amur-leopard (Panthera pardus orle
A:Reference number: A92977
A:Accession: A02373
A:Molecule type: protein
A:Residues: 1-146 <ABB>
C:Comment: In the cat family (Felidae), the oxygen affinity of hemoglobin depends lit
C:Superfamily: globin; globin homology
C:Keywords: acetylated amino end; blood; chromoprotein; erythrocyte; heme; iron; meta
F:3-146/Domain: globin homology <GLB>
F:1/Modified site: acetylated amino end (Ser) #status experimental
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFQRF 10
|||||
Db 32 LVVYPWTFQRF 41

RESULT 88
HBDP2P
hemoglobin beta-II chain - northern Persian leopard
C:Species: Panthera pardus saxicolor (northern Persian leopard)
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000
C:Accession: S03929
R:Ahmed, A.; Jahan, M.; Braunitzer, G.; Goeltenboth, R.
Z. Naturforsch. B 43, 1341-1346, 1988
A:Title: Carnivora: the primary structure of the major and minor hemoglobin component
A:Reference number: S03927
A:Accession: S03929
A:Molecule type: protein
A:Residues: 1-146 <AHM>
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metallopro
F:3-146/Domain: globin homology <GLB>
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFQRF 10
|||||
Db 32 LVVYPWTFQRF 41

RESULT 89

HBU12

hemoglobin beta-II chain - lion

C:Species: Panthera leo (lion)

C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000

C:Accession: S03926

R:Jahan, M.; Ahmed, A.; Braunitzer, G.; Zaidi, Z.H.; Goeltenboth, R.

Z. Naturforsch. B 42, 1465-1470, 1987

A:Title: Carnivora: the primary structures of adult lion (Panthera leo) hemoglobins.

A:Reference number: S03924

A:Accession: S03926

A:Molecule type: protein

A:Residues: 1-146 <JAH>

C:Superfamily: globin; globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metalloprotein

F:3-146/Domain: globin homology <GLB>

F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00017;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
|||||

DB 32 LVVYPWTQRF 41

RESULT 90

HBU10

hemoglobin beta-I chain - jaguar

C:Species: Panthera onca (jaguar)

C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 03-Mar-2000

C:Accession: S00522

R:Ahmed, A.; Jahan, M.; Zaidi, Z.H.; Braunitzer, G.; Goeltenboth, R.

Z. Naturforsch. B 42, 1465-1470, 1987

A:Title: The primary structure of the hemoglobins of the adult jaguar (Panthera onca, CA

A:Reference number: S00521; MUID:88107004

A:Accession: S00522

A:Molecule type: protein

A:Residues: 1-146 <AHM>

A:Note: the sequence of the beta-II chain differs from that shown in having 1-Gly and 13

C:Superfamily: globin; globin homology

C:Keywords: acetylated amino end; blood; chromoprotein; erythrocyte; heme; heterotetramer

F:3-146/Domain: globin homology <GLB>

F:1/Modified site: acetylated amino end (Ser) #status experimental

F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00017;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
|||||

DB 32 LVVYPWTQRF 41

RESULT 91

HBU11

hemoglobin beta-I chain - tiger

C:Species: Panthera tigris sumatrae (Sumatran tiger)

C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000

C:Accession: S02079

R:Jahan, M.; Ahmed, A.; Braunitzer, G.; Goeltenboth, R.

Z. Naturforsch. B 42, 1465-1470, 1987

A:Title: Carnivora: the amino-acid sequence of the adult Sumatran tiger (Panthera tigris

A:Reference number: S02078; MUID:89228545

A:Accession: S02079

A:Molecule type: protein

A:Residues: 1-146 <JAH>

C:Superfamily: globin; globin homology
C:Keywords: acetylated amino end; blood; chromoprotein; erythrocyte; heme; heterotetr
F:3-146/Domain: globin homology <GLB>
F:1/Modified site: acetylated amino end (Ser) #status experimental
F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
|||||

DB 32 LVVYPWTQRF 41

RESULT 92

HBU11

hemoglobin beta-I chain - lion

C:Species: Panthera leo (lion)

C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000

C:Accession: S03925

R:Jahan, M.; Ahmed, A.; Braunitzer, G.; Zaidi, Z.H.; Goeltenboth, R.

Z. Naturforsch. B 42, 1465-1470, 1987

A:Title: Carnivora: the primary structures of adult lion (Panthera leo) hemoglobins.

A:Reference number: S03924

A:Accession: S03925

A:Molecule type: protein

A:Residues: 1-146 <JAH>

C:Superfamily: globin; globin homology

C:Keywords: acetylated amino end; blood; chromoprotein; erythrocyte; heme; heterotetr

F:3-146/Domain: globin homology <GLB>

F:1/Modified site: acetylated amino end (Ser) #status experimental

F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00017;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
|||||

DB 32 LVVYPWTQRF 41

RESULT 93

HBU1P

hemoglobin beta-I chain - northern Persian leopard

C:Species: Panthera pardus saxicolor (northern Persian leopard)

C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000

C:Accession: S03928

R:Ahmed, A.; Jahan, M.; Braunitzer, G.; Goeltenboth, R.

Z. Naturforsch. B 43, 1341-1346, 1988

A:Title: Carnivora: the primary structure of the major and minor hemoglobin component

A:Reference number: S03927

A:Accession: S03928

A:Molecule type: protein

A:Residues: 1-146 <AHM>

C:Superfamily: globin; globin homology

C:Keywords: acetylated amino end; blood; chromoprotein; erythrocyte; heme; heterotetr

F:3-146/Domain: globin homology <GLB>

F:1/Modified site: acetylated amino end (Ser) #status experimental

F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10

Db 32 LVVYPTQRF 41

RESULT 94

HBBX2

hemoglobin beta chain - tiger

C:Species: Panthera tigris sumatrae (Sumatran tiger)

C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000

C:Accession: S11301

R:Jahan, M.; Ahmed, A.; Braunitzer, G.; Goeltenboth, R.

Biol. Chem. Hoppe-Seyler 370, 27-33, 1989

A:Title: Carnivora: the amino-acid sequence of the adult Sumatran tiger (Panthera tigris)

A:Reference number: S02078; MUID:89228545

A:Accession: S11301

A:Molecule type: Protein

A:Residues: 1-146 <JAH>

C:Superfamily: globin; globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metallopro

F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00017;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10

Db 32 LVVYPTQRF 41

RESULT 95

HBBTF

hemoglobin beta chain - Egyptian roussette (tentative sequence)

C:Species: Rousettus aegyptiacus (Egyptian roussette)

C>Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 31-Mar-2000

C:Accession: A02376

R:Kleinschmidt, T.; Braunitzer, G.

Hoppe-Seyler's Z. Physiol. Chem. 363, 1209-1215, 1982

A:Title: Die Primärstruktur des Haemoglobins vom Ägyptischen Flughund (Rousettus aegy

A:Reference number: A91702; MUID:83055089

A:Accession: A02376

A:Molecule type: Protein

A:Residues: 1-146 <KLE>

C:Superfamily: globin; globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier

F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00017;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10

Db 32 LVVYPTQRF 41

RESULT 96

HBBXB

hemoglobin beta chain - black flying fox

C:Species: Pteropus alecto (black flying fox)

C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000

C:Accession: S01309

R:Kleinschmidt, T.; Sgouras, J.G.; Pettigrew, J.D.; Braunitzer, G.

Biol. Chem. Hoppe-Seyler 369, 975-984, 1988

A:Title: The primary structure of the hemoglobin from the grey-headed flying fox (Pterop

A:Reference number: S01308; MUID:89149963

A:Accession: S01309

A:Molecule type: protein

A:Residues: 1-146 <KLE>

A:Note: 139-Thr was also found

C:Superfamily: globin; globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metallopro

F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00017;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10

Db 32 LVVYPTQRF 41

RESULT 97

HBBXG

hemoglobin beta chain - gray-headed flying fox

C:Species: Pteropus poliocephalus (gray-headed flying fox)

C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 03-Mar-2000

C:Accession: S01311

R:Kleinschmidt, T.; Sgouras, J.G.; Pettigrew, J.D.; Braunitzer, G.

Biol. Chem. Hoppe-Seyler 369, 975-984, 1988

A:Title: The primary structure of the hemoglobin from the grey-headed flying fox (Pte

A:Reference number: S01308; MUID:89149963

A:Accession: S01311

A:Molecule type: protein

A:Residues: 1-146 <KLE>

A:Note: 139-Thr was also found

C:Superfamily: globin; globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; heterotetramer; iron; metallopro

F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00017;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10

Db 32 LVVYPTQRF 41

RESULT 98

HBBH

hemoglobin beta chain - western European hedgehog (tentative sequence)

C:Species: Erinaceus europaeus (western European hedgehog)

C>Date: 30-Jun-1979 #sequence_revision 30-Jun-1979 #text_change 31-Mar-2000

C:Accession: A02377

R:Malta, T.; Araya, A.; Matsuda, G.; Goodman, M.

J. Biochem. 85, 259-269, 1979

A:Title: Amino acid sequences of the alpha and beta chains of adult hemoglobin of the

A:Reference number: A91950; MUID:79109529

A:Accession: A02377

A:Molecule type: protein

A:Residues: 1-146 <MAI>

C:Superfamily: globin; globin homology

C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen car

F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted

F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00017;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
 |||||
 DB 32 LVVYPWTORE 41

RESULT 99

HBTSM

hemoglobin beta chain - house shrew (tentative sequence)
 C:Species: Suncus murinus (house shrew)
 C:Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 31-Mar-2000
 C:Accession: A02378
 R:Matra, T.; Matsuda, G.; Takenaka, O.; Takahashi, K.
 Hoppe-Seyler's Z. Physiol. Chem. 362, 1465-1474, 1981
 A:Title: The primary structure of adult hemoglobin of musk shrew (Suncus murinus).
 A:Reference number: A91699; MUID:82074278
 A:Accession: A02378
 A:Molecule type: protein
 A:Residues: 1-146 <MAI>
 C:Superfamily: globin; globin homology
 C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
 F:3-146/Domain: globin homology <GLB>
 F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
 |||||
 DB 32 LVVYPWTORE 41

RESULT 100

HBOBE

hemoglobin beta chain - European mole (tentative sequence)
 C:Species: Talpa europaea (European mole)
 C:Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 31-Mar-2000
 C:Accession: A02379
 R:Kleinschmidt, T.; Jekmann, W.; Braunitzer, G.
 Hoppe-Seyler's Z. Physiol. Chem. 362, 1263-1272, 1981
 A:Title: Die Primärstruktur des Haemoglobins des Maulwurfs (Talpa europaea).
 A:Reference number: A91697; MUID:82263326
 A:Accession: A02379
 A:Molecule type: protein
 A:Residues: 1-146 <KLE>
 C:Superfamily: globin; globin homology
 C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
 F:3-146/Domain: globin homology <GLB>
 F:63/Binding site: oxygen (His) (distal axial ligand) #status predicted
 F:92/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.00017;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
 |||||
 DB 32 LVVYPWTORE 41

Search completed: July 1, 2002, 12:07:10
 Job time: 43 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 1, 2002, 12:07:12 ; Search time 10.33 seconds

(without alignments)
37,483 M.Illion cell updates/sec

Title: US-09-147-490-1

Perfect score: 10

Sequence: 1 LVVYPMWQRF 10

Scoring table: OLIGO

Searched: 105224 seqs, 38719550 residues

Word size: 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	100.0	60	1 HBB_MACCU	P81042 macropus eu
2	10	100.0	141	1 HBB_CAPHI	P02078 capra hircu
3	10	100.0	141	1 HBB_C_SHEEP	P02079 ovis aries
4	10	100.0	145	1 HBB_BOSJA	P04346 bos javanic
5	10	100.0	145	1 HBB_CAPHI	P02077 capra hircu
6	10	100.0	145	1 HBB_BOVIN	P02081 bos taurus
7	10	100.0	145	1 HBB_CAPHI	P02082 capra hircu
8	10	100.0	145	1 HBB_SHEEP	P02083 ovis aries
9	10	100.0	145	1 HBB_ALCAA	P09422 bison bonas
10	10	100.0	145	1 HBB_BISBO	P02071 bos gaurus
11	10	100.0	145	1 HBB_BOSGF	P02072 bos mutus g
12	10	100.0	145	1 HBB_BOSMU	P02079 ovis aries
13	10	100.0	145	1 HBB_BOVIN	P02074 odocoileus
14	10	100.0	145	1 HBB_ODOVI	P02076 ovis orient
15	10	100.0	145	1 HBB_OVTMU	P21380 rangifer ta
16	10	100.0	145	1 HBB_RANTA	P02075 ovis aries
17	10	100.0	145	1 HBB_SHEEP	P04245 tragelaphus
18	10	100.0	145	1 HBB_TRAST	P18987 iguana igua
19	10	100.0	146	1 HBB_IGUIG	P10060 sphendon p
20	10	100.0	146	1 HBB_SPHPU	P02064 tapirus ter
21	10	100.0	146	1 HBB_TAPTE	P18991 uromastix h
22	10	100.0	146	1 HBB_UROHA	P18988 panthera le
23	10	100.0	146	1 HBB_PANLE	P02065 tapirus ter
24	10	100.0	146	1 HBB_TAPTE	P18983 alluropoda
25	10	100.0	146	1 HBB_AILME	P14388 antrozous p
26	10	100.0	146	1 HBB_AILFU	P02035 actus trivi
27	10	100.0	146	1 HBB_ANTPA	P02034 ateles geot
28	10	100.0	146	1 HBB_AORTA	P18984 balenopter
29	10	100.0	146	1 HBB_ATEGE	P18985 callithrix
30	10	100.0	146	1 HBB_BALAC	P02095 cavia porce
31	10	100.0	146	1 HBB_CALAC	P02040 cebus albif
32	10	100.0	146	1 HBB_CAVPO	
33	10	100.0	146	1 HBB_CERAT	

34	10	100.0	146	1 HBB_CERAP	P02041 cebus apell
35	10	100.0	146	1 HBB_CERAE	P02028 ceropithec
36	10	100.0	146	1 HBB_CERST	P02066 ceratotherc
37	10	100.0	146	1 HBB_CERTO	P02031 cercocobus
38	10	100.0	146	1 HBB_COLBA	P02033 colobus bad
39	10	100.0	146	1 HBB_COLPO	P19885 colobus pol
40	10	100.0	146	1 HBB_CROCR	P18986 crocuta cro
41	10	100.0	146	1 HBB_CROCU	P20855 ctenodactyl
42	10	100.0	146	1 HBB_CVNSP	P17154 cynopterus
43	10	100.0	146	1 HBB_DASNO	P02087 dasypus nov
44	10	100.0	146	1 HBB_ECHTE	P24292 echinops te
45	10	100.0	146	1 HBB_EQUHE	P02063 equus hemio
46	10	100.0	146	1 HBB_ERIEU	P02059 erinaceus e
47	10	100.0	146	1 HBB_EULFU	P02053 eulemur ful
48	10	100.0	146	1 HBB_FELCA	P07412 felis silve
49	10	100.0	146	1 HBB_GALCR	P02050 galago cras
50	10	100.0	146	1 HBB_GORGO	P02024 gorilla gor
51	10	100.0	146	1 HBB_HIPAM	P19016 hippopotamu
52	10	100.0	146	1 HBB_HORSE	P02062 equus cabal
53	10	100.0	146	1 HBB_HUMAN	P02023 homo sapien
54	10	100.0	146	1 HBB_HYLLA	P02025 hylobates l
55	10	100.0	146	1 HBB_LEMCA	P02025 lemur catia
56	10	100.0	146	1 HBB_LEMVA	P21667 lemur varie
57	10	100.0	146	1 HBB_LEPEU	P08535 lepus europ
58	10	100.0	146	1 HBB_LERPE	P15166 leptomyscot
59	10	100.0	146	1 HBB_LORTA	P02048 loris tard
60	10	100.0	146	1 HBB_LORTU	P10893 loris tard
61	10	100.0	146	1 HBB_LYMLY	P41328 lynx lynx (
62	10	100.0	146	1 HBB_MACCA	P09840 macrotus ca
63	10	100.0	146	1 HBB_MACFU	P02027 macaca fusc
64	10	100.0	146	1 HBB_MACGS	P24660 macrodema
65	10	100.0	146	1 HBB_MANSF	P08259 mandrillus
66	10	100.0	146	1 HBB_MARMA	P08853 marota mar
67	10	100.0	146	1 HBB_MEGLY	P11752 megalocera l
68	10	100.0	146	1 HBB_MELCA	P15449 mellivora c
69	10	100.0	146	1 HBB_MESAU	P02094 mesocricetu
70	10	100.0	146	1 HBB_MUSLU	P23602 muscicela jut
71	10	100.0	146	1 HBB_MUSPF	P19017 muscicela put
72	10	100.0	146	1 HBB_MYOVE	P11758 myotis vell
73	10	100.0	146	1 HBB_NASNA	P26916 nasua nasua
74	10	100.0	146	1 HBB_NYCCO	P02049 nycticebus
75	10	100.0	146	1 HBB_ODORO	P10779 odobenus ro
76	10	100.0	146	1 HBB_ONDZ1	P02093 ondatra zib
77	10	100.0	146	1 HBB_ORNAN	P02111 ornithorhyn
78	10	100.0	146	1 HBB_PAGLA	P19646 paguma latv
79	10	100.0	146	1 HBB_PANPO	P04244 panthera pa
80	10	100.0	146	1 HBB_PANTO	P10884 panthera tl
81	10	100.0	146	1 HBB_PAPCY	P02030 phoca cynoc
82	10	100.0	146	1 HBB_PHOVI	P09909 phoca vitul
83	10	100.0	146	1 HBB_PHYCA	P09605 physeter ca
84	10	100.0	146	1 HBB_PIG	P02067 sus scrofa
85	10	100.0	146	1 HBB_PREN	P02032 presbytis e
86	10	100.0	146	1 HBB_PROCR	P23020 procavia cr
87	10	100.0	146	1 HBB_PROHA	P02086 procavia ca
88	10	100.0	146	1 HBB_PROLO	P18989 procavia lot
89	10	100.0	146	1 HBB_PTEAL	P14391 pteropus al
90	10	100.0	146	1 HBB_PTEBR	P10886 pteronura b
91	10	100.0	146	1 HBB_PTEPO	P14392 pteropus po
92	10	100.0	146	1 HBB_RABIT	P02057 coryctolagus
93	10	100.0	146	1 HBB_RHUN	P09907 rhinoceros
94	10	100.0	146	1 HBB_RHUNE	P02058 rhinoceros a
95	10	100.0	146	1 HBB_SAGFU	P02039 saginus fu
96	10	100.0	146	1 HBB_SAGMY	P02038 saginus my
97	10	100.0	146	1 HBB_SAGNI	P02037 saginus ni
98	10	100.0	146	1 HBB_SALAC	P02036 salmistr sci
99	10	100.0	146	1 HBB_SPAEH	P02090 spallax leuc
100	10	100.0	146	1 HBB_SPECI	P09421 spermophilu

ALIGNMENTS

RESULT 1

```

HBE_MACEU
ID HBE_MACEU STANDARD: PRT; 60 AA.
AC P81042:
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Hemoglobin epsilon chain (Fragment).
CN HBE1.
OS Macropus eugenii (Tamar wallaby).
OC Mammalia; Metatheria; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315;
RN [1]
RP SEQUENCE.
RC TISSUE=Blood;
RX MEDLINE=98000287; PubMed=9342240;
RA Holland R.A.B., Gooley A.A.;
RT "Characterization of the embryonic globin chains of the marsupial
Tamar wallaby, Macropus eugenii."
RL Eur. J. Biochem. 248:864-871(1997).
CC -1- FUNCTION: HEMOGLOBIN EPSILON CHAIN IS A EMBRYONIC-TYPE BETA-TYPE
CHAIN FOUND IN PRENATAL AND NEONATAL MARSUPIALS.
DR HSSP: F02100; IASM.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin.1.
DR PROSITE: PS01033; GLOBIN.1.
KW Heme: Oxygen transport; Transport; Erythrocyte.
FT NON_TER 60
SQ SEQUENCE 60 AA; 6510 MW; C3CF20BC445C649C CRC64;

Query Match 100.0%; Score 10; DB 1; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWQRF 10
DB 32 LVVYPWQRF 41

RESULT 2
HBBQ_CAPHI
ID HBBQ_CAPHI STANDARD: PRT; 141 AA.
AC P02078:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta-C chain (Cysteine-beta).
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82137075; PubMed=6277503;
RA Schon E.A., Cleary M.L., Haynes J.R., Lingrel J.B.;
RT "Structure and evolution of goat gamma-, beta C- and beta A-globin
genes: three developmentally regulated genes contain inserted
elements."
RL Cell 27:359-369(1981).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -1- MISCELLANEOUS: THIS TYPE OF BETA-C CHAIN IS FOUND WHEN ANEMIA HAS
BEEN EXPERIMENTALLY PRODUCED.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
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CC or send an email to license@isb-sib.ch).
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DR EMBL: M15389; AAA30914.1; ALT_SEQ.
DR PIR: A02396; HBGT.
DR HSSP: P02070; HDA.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin.1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN.1.
KW Heme: Oxygen transport; Transport; Erythrocyte.
FT INIT_MET 0
FT METAL 58 58 IRON (HEME DISTAL LIGAND).
FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 141 AA; 15620 MW; 305CEA482FAC825C CRC64;

Query Match 100.0%; Score 10; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWQRF 10
DB 27 LVVYPWQRF 36

RESULT 3
HBBQ_SHEEP
ID HBBQ_SHEEP STANDARD: PRT; 141 AA.
AC P02679:
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Hemoglobin beta-C chain.
OS Ovis aries (Sheep).
OS Ovis orientalis musimon (Mouflon), and
OS Ammotragus lervia (Barbary sheep) (Aoudad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940, 9938, 9899;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Sheep.
RX MEDLINE=89178744; PubMed=2494347;
RA Garner K.D., Lingrel J.B.;
RT "A comparison of the beta A- and beta B-globin gene clusters of
sheep."
RL J. Mol. Evol. 28:175-184(1989).
RN [2]
RP SEQUENCE.
RC SPECIES=Sheep.
RX MEDLINE=67134347; PubMed=6022868;
RA Boyer S.H., Hathaway P., Pascasio F., Bordley J., Orton C.,
RA Naughton M.A.;
RT "Differences in the amino acid sequences of tryptic peptides from
three sheep hemoglobin beta chains."
RL J. Biol. Chem. 242:2211-2232(1967).
RN [3]
RP SEQUENCE.
RC SPECIES=Sheep.
RA Wilson J.B., Edwards W.C., McDaniel M., Dobbs M.M., Huismann T.H.J.;
RT "The structure of sheep hemoglobins. II. The amino acid composition
of the tryptic peptides of the non-alpha chains of hemoglobins A, B,
C, and F."
RL Arch. Biochem. Biophys. 115:385-400(1966).
RN [4]
RP COMPOSITION OF TRYPTIC PEPTIDES EXCEPT POSITIONS 100-111.
RC SPECIES=O. musimon, and A. lervia.
RX MEDLINE=71089262; PubMed=5496230;
RA Wilson J.B., Miller A., Huismann T.H.J.;

```

RT "Production of hemoglobin C in the Mouflon (Ovis musimon Pallas, 1811) and the Barbary sheep (Ammotragus lervia Pallas, 1777) during experimental anemia: amino acid composition of tryptic peptides from the beta B and bet C chains." ;

RT Blochem. Genet. 4:677-688(1970).

CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.

CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.

CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.

CC -1- MISCELLANEOUS: THIS TYPE OF BETA-C CHAIN IS FOUND IN THESE ANIMALS WHEN ANEMIA HAS BEEN EXPERIMENTALLY PRODUCED.

CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

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DR EMBL: X14728; CA32850.1; -.

DR PIR: A02396; HBSHC.

DR PIR: A02396; HBMEC.

DR PIR: A02396; HBSHCR.

DR PIR: S10074; S10074.

DR HSSP: P02070; 1HDA.

DR InterPro: IPR002337; Beta_haem.

DR InterPro: IPR000971; Globin.

DR Pfam: PF00042; globin; 1.

DR PRINTS: PR00814; BETAHEM.

DR PROSITE: PS01033; GLOBIN; 1.

KW Heme; Oxygen transport; Transport; Erythrocyte.

FT INIT_MER 0 0

FT METAL 58 58 IRON (HEME DISTAL LIGAND).

FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).

FT VARIANT 68 68 N -> Z (IN BARBARY SHEEP).

FT CONFLICT 82 82 Q -> E (IN REF. 3)

SQ SEQUENCE 141 AA; 15619 MW; 3409EDB54528C358 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
|||||
DB 27 LVVYPWTQRF 36

RESULT 4
ID HBA_BOSJA STANDARD; PRT; 145 AA.
AC P04346;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta-A chain.
OS Bos javanicus (Wild banteng).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9906;
RN NCBI_TaxID=9906;
RP SEQUENCE.
RC STRAIN=HEREFORD;
RX MEDLINE=84023669; PubMed=6626147;
RA Namikawa T., Takenaka O., Takahashi K.;
RT "Hemoglobin Bali (bovine): beta A 18(Bl)lys leads to his: one of the missing links between beta A and beta B of domestic cattle exists in the Bali cattle (Bovinae, Bos banteng).";
RL Blochem. Genet. 21:787-796(1983).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE

CC VARIOUS PERIPHERAL TISSUES.

CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.

CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.

CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

DR PIR: A02388; HBBOB.

DR HSSP: P02070; 1HDA.

DR InterPro: IPR002337; Beta_haem.

DR InterPro: IPR000971; Globin.

DR Pfam: PF00042; globin; 1.

DR PRINTS: PR00814; BETAHEM.

DR PROSITE: PS01033; GLOBIN; 1.

KW Heme; Oxygen transport; Transport; Erythrocyte.

FT METAL 62 62 IRON (HEME DISTAL LIGAND).

FT METAL 91 91 IRON (HEME PROXIMAL LIGAND).

SQ SEQUENCE 145 AA; 15964 MW; 52685BDC8CDFBD5 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
|||||
DB 31 LVVYPWTQRF 40

RESULT 5
ID HBA_CAPHI STANDARD; PRT; 145 AA.
AC P02077;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Hemoglobin beta-A chain (Alanine-beta).
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Capra.
OC NCBI_TaxID=9925;
RN NCBI_TaxID=9925;
RP SEQUENCE FROM N.A.
RX MEDLINE=82137075; PubMed=6277503;
RA Schon E.A., Cleary M.L., Haynes J.R., Lingrel J.B.;
RT "Structure and evolution of goat gamma-, beta C- and beta A-globin genes: three developmentally regulated genes contain inserted elements." ;
RT Cell 27:359-369(1981).
RN [2]
RP PARTIAL SEQUENCE (ALTELE A).
RX MEDLINE=67165362; PubMed=6026247;
RA Huisman T.H.J., Adams H.R., Dimmock M.O., Edwards W.E., Wilson J.B.;
RT "The structure of goat hemoglobins. I. Structural studies of the beta chains of the hemoglobins of normal and anemic goats." ;
RL J. Biol. Chem. 242:2534-2541(1967).
RN [3]
RP PARTIAL SEQUENCE (ALTELE D).
RX MEDLINE=69036192; PubMed=5697993;
RA Adams H.R., Boyd E.M., Wilson J.B., Miller A., Huisman T.H.J.;
RT "The structure of goat hemoglobins. 3. Hemoglobin D, a beta chain variant with one apparent amino acid substitution (21 Asp-->His).";
RL Arch. Biochem. Biophys. 127:398-405(1968).
RN [4]
RP PARTIAL SEQUENCE (ALTELE E).
RX MEDLINE=70252721; PubMed=5433580;
RA Wrightstone R.N., Wilson J.B., Miller A., Huisman T.H.J.;
RT "The structure of goat hemoglobins. IV. A third beta chain variant (betaE) with three apparent amino acid substitutions." ;
RL Arch. Biochem. Biophys. 138:451-456(1970).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -1- POLYMORPHISM: THERE ARE AT LEAST ALLELES. THE SEQUENCE SHOWN IS

```
CC      THAT OF ALLELE A.
CC      -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
CC      -----
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CC      or send an email to license@lsb-sib.ch).
CC      -----
DR      EMBL; M1587; AAA30913.1; -.
DR      PIR; A02395; HBGTA.
DR      HSSP; P02070; 1HDA.
DR      InterPro; IPR002337; Beta_haem.
DR      InterPro; IPR000971; Globin.
DR      Pfam; PF00042; globin; 1.
DR      PRINTS; PR00814; BETAHAEM.
DR      PROSITE; PS01033; GLOBIN; 1.
KW      Heme; Oxygen transport; Transport; Erythrocyte;
KW      Polymorphism.
FT      METAL           62      62      IRON (HEME DISTAL LIGAND).
FT      METAL           91      91      IRON (HEME PROXIMAL LIGAND).
FT      VARIANT         20      20      D -> H (IN ALLELE D).
FT      VARIANT         86      86      Q -> H (IN ALLELE E).
FT      VARIANT        103      103      K -> R (IN ALLELE E).
FT      VARIANT        124      124      L -> V (IN ALLELE E).
SQ      SEQUENCE      145 AA; 16021 MW; 6C59F105A940F4D0 CRC64;

Query Match      100.0%; Score 10; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 LVYPMWTFORF 10
        |||
        31 LVYPMWTFORF 40

RESULT 6
ID      HBBF_BOVIN      STANDARD;      PRT;      145 AA.
AC      P02081;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Hemoglobin beta fetal chain (Hemoglobin gamma chain).
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Bovinae; Bos.
OX      NCBI_TaxID=9913;
[1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=84144058; PubMed=6322113;
RA      Schimenti J.C., Duncan C.H.;
RT      "Ruminant globin gene structures suggest an evolutionary role for
RT      Alu-type repeats."
RL      Nucleic Acids Res. 12:1641-1655(1984).
[2]
RN      SEQUENCE.
RP      MEDLINE=67089183; PubMed=5958205;
RA      Babin D.R., Schroeder W.A., Shelton J.R., Roberson B.;
RT      "The amino acid sequence of the gamma chain of bovine fetal
RT      hemoglobin."
RL      Biochemistry 5:1297-1310(1966).
[3]
CC      -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC      VARIOUS PERIPHERAL TISSUES.
CC      -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC      -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC      -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
CC      -----
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CC      or send an email to license@lsb-sib.ch).
CC      -----
DR      EMBL; X00354; CAA25101.1; -.
DR      EMBL; M63452; AAA30519.1; -.
DR      PIR; A02398; HBBOF.
DR      HSSP; P02070; 1HDA.
DR      InterPro; IPR002337; Beta_haem.
DR      InterPro; IPR000971; Globin.
DR      Pfam; PF00042; globin; 1.
DR      PRINTS; PR00814; BETAHAEM.
DR      PROSITE; PS01033; GLOBIN; 1.
KW      Heme; Oxygen transport; Transport; Erythrocyte.
FT      METAL           62      62      IRON (HEME DISTAL LIGAND).
FT      METAL           91      91      IRON (HEME PROXIMAL LIGAND).
SQ      SEQUENCE      145 AA; 15859 MW; 78B8722915E9C221 CRC64;

Query Match      100.0%; Score 10; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 LVYPMWTFORF 10
        |||
        31 LVYPMWTFORF 40

RESULT 7
ID      HBBF_CAPRI      STANDARD;      PRT;      145 AA.
AC      P02082;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Hemoglobin beta fetal chain (Hemoglobin gamma chain).
OS      Capra hircus (Goat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Caprinae; Capra.
OX      NCBI_TaxID=9925;
[1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=82137075; PubMed=6277503;
RA      Schon E.A., Cleary M.L., Haynes J.R., Lingrel J.B.;
RT      "Structure and evolution of goat gamma-, beta C- and beta A-globin
RT      genes: three developmentally regulated genes contain inserted
RT      elements."
RL      Cell 27:359-369(1981).
[2]
RN      SEQUENCE.
RP      MEDLINE=83005406; PubMed=7118074;
RX      Kleinschmidt T., Braunitzer G.;
RT      "The primary structure of the hemoglobin gamma-chains of fetal sheep
RT      (Ovis aemon) and goat (Capra aegagrus). Artiodactyla."
RL      Hoppe-Seyler's Z. Physiol. Chem. 353:769-796(1982).
[3]
RP      SEQUENCE OF 52-97 FROM N.A.
RX      MEDLINE=80227766; PubMed=6248519;
RA      Haynes J.R., Rostock P.R., Schon E.A., Gallagher P.M., Burks D.J.,
RA      Smith K., Lingrel J.B.;
RT      "The isolation of the beta A-, beta C-, and gamma-globin genes and a
RT      presumptive embryonic globin gene from a goat DNA recombinant
RT      library."
RL      J. Biol. Chem. 255:6355-6367(1980).
[4]
CC      -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC      VARIOUS PERIPHERAL TISSUES.
CC      -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC      -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC      -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
CC      -----
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DR EMBL; M15388; AAA30925.1; -.
DR EMBL; K00663; AAA30923.1; -.
DR PIR; A02399; HBGF.
DR HSSP; P02070; 1HDA.
DR InterPro; IPR002337; Beta_haem.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport; Erythrocyte.
FT METAL 62 62 IRON (HEME DISTAL LIGAND).
FT METAL 91 91 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 145 AA; 15946 MW; E143C91CC898652 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPTQRF 10
   |||||
Db 31 LVVYPTQRF 40

RESULT 8
HBBF_SHEEP STANDARD; PRT; 145 AA.
ID HBBF_SHEEP
AC P02083;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Hemoglobin beta fetal chain (Hemoglobin gamma chain).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE OF 1-29; 52-96 AND 104-145 FROM N.A.
RA MEDLINE=81117290; PubMed=6161931;
RA Kretscher P.J., Coon H.C., Davis A., Harrison M., Nienhuis A.W.;
RT "Hemoglobin switching in sheep. Isolation of the fetal gamma-globin
gene and demonstration that the fetal gamma- and adult beta A-globin
genes lie within eight kilobase segments of homologous DNA."
RL J. Biol. Chem. 256:1975-1982(1981).
RN [2]
RP SEQUENCE.
RA MEDLINE=77022158; PubMed=974104;
RA Dardre P.D., Lehmann H.;
RT "The gamma chain of the lamb."
RL Blochm. Biophys. Acta 446:10-18(1976).
CC -1 SUBUNIT: HETEROPTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1 SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
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or send an email to license@isb-sib.ch).
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DR EMBL; K02824; AAA31533.1; -.
DR EMBL; K02825; AAA31534.1; -.

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DR EMBL; K02826; AAA31535.1; -.
DR PIR; A92306; HGSB.
DR HSSP; P02070; 1HDA.
DR InterPro; IPR002337; Beta_haem.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport; Erythrocyte.
FT METAL 62 62 IRON (HEME DISTAL LIGAND).
FT METAL 91 91 IRON (HEME PROXIMAL LIGAND).
FT CONFLICT 119 120 GE -> EG (IN REF. 2).
SQ SEQUENCE 145 AA; 15931 MW; 9924A27CCBC34C28 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPTQRF 10
   |||||
Db 31 LVVYPTQRF 40

RESULT 9
HBB_ALCAHA STANDARD; PRT; 145 AA.
ID HBB_ALCAHA
AC P02073;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta chain.
OS Alces alces alces (European moose) (Elk).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervidae; Odocoileinae; Alces.
OX NCBI_TaxID=9853;
RN [1]
RP SEQUENCE.
RA MEDLINE=85078042; PubMed=6510898;
RA Aschauer H., Wiesner H., Braunitzer G.;
RT "Intrinsic oxygen affinity: the primary structure of a ruminantia
hemoglobin: methionine in betaNA2 of a pecora, the Northern elk
(Alces alces alces)."
RL Hope-Seyley's Z. Physiol. Chem. 365:1323-1330(1984).
CC -1 FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC VARIOUS PERIPHERAL TISSUES.
CC -1 SUBUNIT: HETEROPTRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1 TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -1 SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR PIR; A02392; HBKN.
DR HSSP; P02070; 1HDA.
DR InterPro; IPR002337; Beta_haem.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport; Erythrocyte.
FT METAL 62 62 IRON (HEME DISTAL LIGAND).
FT METAL 91 91 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 145 AA; 16223 MW; C2D22F363B78EA CRC64;

Query Match 100.0%; Score 10; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPTQRF 10
   |||||
Db 31 LVVYPTQRF 40

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RESULT 10
HBB_BISBO STANDARD; PRT; 145 AA.
ID AC P09422;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta chain.
GN HBB.
OS Bison bonasus (European bison).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bison.
OX NCBI_TaxID=9902;
RN [1]
RP SEQUENCE.
RX MEDLINE=86296178; PubMed=3741621;
RA Mazur G., Mueller E., Braunltzer G., Wiesner H.;
RT "Intrinsic oxygen affinity of hemoglobins: the hemoglobin of bison
RT (Bison bonasus, Bovidae).";
RL Biol. Chem. Hoppe-Seyler 367:417-423(1986).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR HSSP: P02070; 1HDA.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin.1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN: 1.
KM Heme; Oxygen transport; Transport; Erythrocyte.
FT METAL 62 62 IRON (HEME DISTAL LIGAND).
FT METAL 91 91 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 145 AA; 15976 MW; 4634F52EC1772BA3 CRC64;

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Query Match 100.0%; Score 10; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 LVVYPTQRF 10
    |||||
Db 31 LVVYPTQRF 40

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RESULT 11
HBB_BOSGF STANDARD; PRT; 145 AA.
ID AC P02071;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta chain.
GN HBB.
OS Bos gaurus frontalis (Gayal), and
OS Bubalus bubalis (domestic water buffalo).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=30520, 89462;
RN [1]
RP SEQUENCE.
RX MEDLINE=85005246; PubMed=6479895;
RA Lalithanluanga R., Brauntlzer G.;
RT "Amino-acid sequence of gayal hemoglobin (Bos gaurus frontalis,
RT Bovidae).";
RL Hoppe-Seyler's Z. Physiol. Chem. 365:737-741(1984).
RN [2]
RP SEQUENCE.

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RC SPECIES=B.bubalis;
RX MEDLINE=92362189; PubMed=1499282;
RA Ferranti P., di Luccia A., Malorni A., Pucci P., Ruoppolo M.,
RA Marino G., Ferrara L.;
RT "River buffalo (Bubalus bubalis L.) AA phenotype haemoglobins:
RT characterization by immobilized polyacrylamide gel electrophoresis and
RT high performance liquid chromatography and determination of the
RT primary structure of the constitutive chains by mass spectrometry.";
RL Comp. Biochem. Physiol. 101B:91-98(1992).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR PIR: A02389; HBBOS.
DR PIR: A49141; AA9141.
DR HSSP: P02070; 1HDA.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin.1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN: 1.
KM Heme; Oxygen transport; Transport; Erythrocyte.
FT METAL 62 62 IRON (HEME DISTAL LIGAND).
FT METAL 91 91 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 145 AA; 15986 MW; 5260F17E84737FB3 CRC64;

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Query Match 100.0%; Score 10; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 LVVYPTQRF 10
    |||||
Db 31 LVVYPTQRF 40

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RESULT 12
HBB_BOSMU STANDARD; PRT; 145 AA.
ID AC P02072;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta chain.
GN HBB.
OS Bos mutus grunniens (Yak).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=30521;
RN [1]
RP SEQUENCE (BETA-I AND BETA-II ALLELES).
RX MEDLINE=85225945; PubMed=4005038;
RA Lalithanluanga R., Wiesner H., Brauntlzer G.;
RT "Studies on yak hemoglobin (Bos grunniens, Bovidae): structural basis
RT for high intrinsic oxygen affinity?";
RL Biol. Chem. Hoppe-Seyler 366:63-68(1985).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -1- POLYMORPHISM: THE BETA-II ALLELE IS SHOWN, IT OCCURS MUCH MORE
CC FREQUENTLY THAN THE BETA-I ALLELE.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR PIR: A02390; HBYA2.
DR HSSP: P02070; 1HDA.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin.1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN: 1.
KM Heme; Oxygen transport; Transport; Erythrocyte;

```

KW Polymorphism. 62 62 IRON (HEME DISTAL LIGAND).
 FT METAL 62 91 IRON (HEME PROXIMAL LIGAND).
 FT VARIANT 49 49 S -> T (IN BETA-I ALLELE).
 FT VARIANT 116 116 H -> N (IN BETA-I ALLELE).
 FT VARIANT 134 134 V -> A (IN BETA-I ALLELE).
 SQ SEQUENCE 145 AA; 15991 MM; F937353D4A65F5AA2 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 145;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVYPTWTF 10
 31 LVVYPTWTF 40

RESULT 13
 HBB_BOVIN STANDARD; PRT; 145 AA.
 AC P02070.
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 NC NCB1_TaxID=9913;
 RX MEDLINE=68144058; PubMed=6322113;
 RA Schimenti J.C., Duncan C.H.;
 RT "Ruminant globin gene structures suggest an evolutionary role for
 RT Alu-type repeats."
 RL Nucleic Acids Res. 12:1641-1655(1984).
 RN [2]
 RP SEQUENCE (ALLELES A AND B).
 RX MEDLINE=68001834; PubMed=6048711;
 RA Schroeder W.A., Shelton J.R., Roberson B., Babin D.R.;
 RT "A comparison of amino acid sequences in the beta-chains of adult
 RT bovine hemoglobins A and B."
 RL Arch. Biochem. Biophys. 120:124-135(1967).
 RN [3]
 RP PARTIAL SEQUENCE (ALLELES C-RHODESIA AND D-ZAMBIA).
 RX MEDLINE=73007895; PubMed=4561255;
 RA Schroeder W.A., Shelton J.R., Shelton J.B., Apell G., Huisman T.H.J.,
 RT Smith L.L., Carr W.R.;
 RT "Amino acid sequences in the beta-chains of adult bovine hemoglobins
 RT C-Rhodesia and D-Zambia."
 RL Arch. Biochem. Biophys. 152:222-232(1972).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=94016570; PubMed=8411160;
 RA Perutz M.F., Fermi G., Poyart C., Pagnier J., Kister J.;
 RT "A novel allosteric mechanism in haemoglobin. Structure of bovine
 RT deoxyhaemoglobin, absence of specific chloride-binding sites and
 RT origin of the chloride-linked Bohr effect in bovine and human
 RT haemoglobin."
 RL J. Mol. Biol. 233:536-545(1993).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RX MEDLINE=21262557; PubMed=11369847;
 RA Sato M.K., Abraham D.J.;
 RT "The X-ray structure determination of bovine carboxymonoxy hemoglobin
 RT at 2.1 A resolution and its relation to the quaternary structures
 RT of other hemoglobin crystal forms."
 RL Protein Sci. 10:1091-1099(2001).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.

CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- POLYMORPHISM: FOUR ALLELIC BETA CHAINS HAVE BEEN FOUND IN BOVINE
 CC HEMOGLOBINS. A AND B ALLELES WERE FOUND IN JERSEY CATTLE AND C
 CC AND D ALLELES WERE FOUND IN ANGONI CATTLE (EAST AFRICAN SHORT-HORN
 CC ZEBU). THE SEQUENCE SHOWN IS THAT OF THE ALLELE A.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 CC -1- DATABASE: NAME=Washington enzyme manual;
 CC WWW="http://www.washington-biochem.com/manual/H/HB.html".

CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@sdb.ch).
 CC -----

DR EMBL: X00376; CAA25111.1;
 DR EMBL: M63453; AAA30408.1;
 DR PIR: A02387; HBBOB.
 DR PDB: 1HDA; 31-MAY-94.
 DR PDB: 1FSX; 06-JUN-00.
 DR InterPro: IPR002337; Beta.haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte;
 KW Polymorphism; 3D-structure.

FT METAL 62 62 IRON (HEME DISTAL LIGAND).
 FT VARIANT 91 91 IRON (HEME PROXIMAL LIGAND).
 FT VARIANT 15 15 G -> S (IN ALLELE B).
 FT VARIANT 18 18 K -> H (IN ALLELE B).
 FT VARIANT 20 20 D -> G (IN ALLELE D-ZAMBIA).
 FT VARIANT 43 43 S -> T (IN ALLELE D-ZAMBIA).
 FT VARIANT 119 119 K -> N (IN ALLELE B).
 FT VARIANT 131 131 K -> Q (IN ALLELE C-RHODESIA).
 SQ SEQUENCE 145 AA; 15954 MM; F862217E8477CFD4 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 145;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVYPTWTF 10
 31 LVVYPTWTF 40

RESULT 14
 HBB_ODOVI STANDARD; PRT; 145 AA.
 AC P02074.
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Hemoglobin beta-III chain.
 GN HBB.
 OS Odocoileus virginianus virginianus (Virginia white-tailed deer).
 CC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
 CC Cervidae; Odocoileinae; Odocoileus.
 NC NCB1_TaxID=9875;
 RX MEDLINE=83185439; PubMed=6841126;
 RA Shimizu K., Wong S.C., Wilson J.B., Lam H., Reynolds A.E., Singh P.,
 RA Huisman T.H.J., Charles N.G., Amma E.L.;
 RT "The primary sequence of the beta chain of Hb type III of the
 RT Virginia white-tailed deer (Odocoileus virginianus), a comparison with
 RT putative sequences of the beta chains from four additional deer
 RT hemoglobins, types II, IV, V, and VIII, and relationships between

RT Intermolecular contacts, primary sequence and sickling of deer
 RT hemoglobins.";
 RL Hemoglobin 7:15-45(1983).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (1.98 ANGSTROMS).
 RA Schmidt W.C. Jr., Girling R.L., Houston T.E., Sproul G.D., Amma E.L.,
 RA Huisman T.H.J.;
 RA "The structure of sickling deer type III hemoglobin by molecular
 RT replacement.";
 RL Acta Crystallogr. B 33:335-342(1977).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- POLYMORPHISM: THIS CHAIN IS ONE OF FIVE BETA CHAIN ALLELES.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 CC -1- CAUTION: THERE ARE CONFLICTS WITH THE SEQUENCE STORED IN PDB.
 DR PIR: A02393; HBDE3.
 DR PDB: 1HDS; 30-SEP-83.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte;
 KW 3D-structure.
 FT METAL 62 62 IRON (HEME DISTAL LIGAND).
 FT METAL 91 91 IRON (HEME PROXIMAL LIGAND).
 FT TURN 4 5
 FT HELIX 6 13
 FT TURN 14 16
 FT TURN 20 21
 FT HELIX 22 30
 FT TURN 31 33
 FT TURN 35 36
 FT TURN 38 40
 FT HELIX 41 43
 FT HELIX 50 55
 FT TURN 57 57
 FT HELIX 58 65
 FT TURN 66 66
 FT TURN 68 72
 FT TURN 85 86
 FT HELIX 87 93
 FT TURN 94 95
 FT HELIX 99 117
 FT TURN 119 120
 FT HELIX 123 142
 SQ SEQUENCE 145 AA; 15824 MW; F3875A54C4C84323 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 145;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10
 |||||||||
 DB 31 LVVYPTQRF 40

RESULT 15
 HBB_OVIMU STANDARD; PRT; 145 AA.
 AC P02076;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Ovis orientalis musimon (Mouflon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.

OX NCBI_TaxID=9938;
 RN [1]
 RP SEQUENCE OF 1-103 AND 116-145.
 RX MEDLINE=71089262; PubMed=5496230;
 RA Wilson J.B., Miller A., Huisman T.H.J.;
 RA "Production of hemoglobin C in the Mouflon (Ovis musimon Pallas,
 RT 1811) and the Barbary sheep (Ammotragus lervia Pallas, 1777) during
 RT experimental anemia: amino acid composition of tryptic peptides from
 RT the beta B and bet C chains.";
 RL Blochem. Genet. 4:677-688(1970).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- MISCELLANEOUS: THIS BETA CHAIN IS TERMED THE B ALLELE, EVEN THOUGH
 CC IT MORE CLOSELY RESEMBLES THE SHEEP A ALLELE.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: S16377; S16377.
 DR HSSP: P02070; 1HDA.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 KW METAL 62 62 IRON (HEME DISTAL LIGAND).
 FT METAL 91 91 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 145 AA; 16108 MW; 50C7CDBB8AD3F5DD CRC64;

Query Match 100.0%; Score 10; DB 1; Length 145;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10
 |||||||||
 DB 31 LVVYPTQRF 40

RESULT 16
 HBB_RANTA STANDARD; PRT; 145 AA.
 ID HBB_RANTA
 AC P21380;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Rangifer tarandus (Reindeer) (Caribou).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
 OC Cervidae; Odocoileinae; Rangifer.
 OX NCBI_TaxID=9870;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91152092; PubMed=1998722;
 RA Petruzzelli R., Barra D., Bossa F., Brix O., Nuutinen M.,
 RA Giardina B.;
 RA "The primary structure of hemoglobin from reindeer (Rangifer tarandus
 RT tarandus) and its functional implications.";
 RL Biochim. Biophys. Acta 1076:221-224(1991).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: S13609; S13609.
 DR HSSP: P02070; 1HDA.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHEM.
 DR PROSITE: PS01033; GLOBIN; 1.

KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 62 IRON (HEME DISTAL LIGAND).
 FT METAL 91 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 145 AA; 16166 MW; 53B625CACA1EB1A9 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 145;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10
 |||||
 DB 31 LVVYPTQRF 40

RESULT 17
 HBB_SHEEP STANDARD; PRT; 145 AA.
 AC P02075;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN (1)
 RP SEQUENCE FROM N.A. (B ALLELE).
 RX MEDLINE=89178744; PubMed=2494347;
 RA Garner K.J., Lingrel J.B.;
 RT "A comparison of the beta A-and beta B-globin gene clusters of
 sheep.";
 RT J. Mol. Evol. 28:175-184(1989).
 RN (2)
 RP SEQUENCE (B ALLELE).
 RX MEDLINE=67134347; PubMed=6022868;
 RA Boyer S.H., Hathaway P., Pascasio F., Bordley J., Orton C.,
 RA Naughton M.A.;
 RT "Differences in the amino acid sequences of tryptic peptides from
 three sheep hemoglobin beta chains.";
 RT J. Biol. Chem. 242:2211-2232(1967).
 RN (3)
 RP SEQUENCE OF 1-29; 39-59; 72-85 AND 104-145 FROM N.A. (A ALLELE).
 RX MEDLINE=81117290; PubMed=6161931;
 RA Kretscher P.J., Coon H.C., Davis A., Harrison M., Nienhuis A.W.;
 RT "Hemoglobin switching in sheep. Isolation of the fetal gamma-globin
 gene and demonstration that the fetal gamma- and adult beta A-globin
 genes lie within eight kilobase segments of homologous DNA.";
 RT J. Biol. Chem. 256:1975-1982(1981).
 RN (4)
 RP SEQUENCE OF 1-28 FROM N.A. (B ALLELE).
 RX MEDLINE=88216150; PubMed=3367782;
 RA Garner K.J., Lingrel J.B.;
 RT "Structural organization of the beta-globin locus of B-haplotype
 sheep.";
 RT Mol. Biol. Evol. 5:134-140(1988).
 RN (5)
 RP VARIANT A ALLELE.
 RX MEDLINE=67209244; PubMed=6033754;
 RA Beale D.;
 RT "A partial amino acid sequence for sheep haemoglobin A.";
 RT Biochem. J. 103:129-140(1967).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- POLYMORPHISM: SHEEP HAS TWO ALLELIC BETA CHAINS, A AND B. THE B
 CC ALLELE SEQUENCE IS SHOWN.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

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DR EMBL: X14721; CAA32849.1; -
 DR EMBL: M19754; AAA31528.1; -
 DR EMBL: K02820; AAA31529.1; -
 DR EMBL: K02821; AAA31530.1; -
 DR EMBL: K02822; AAA31531.1; -
 DR EMBL: K02823; AAA31532.1; -
 DR PIR: A02394; HBSHB.
 DR PIR: A94556; HBSHA.
 DR PIR: S10073; S10073.
 DR HSSP: P02070; 1HDA.
 DR InterPro: IPR002337; Beta haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin.1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN: 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte;
 KM Polymorphism.
 FT METAL 62 62
 FT METAL 91 91
 FT VARIANT 49 49
 FT VARIANT 57 57
 FT VARIANT 74 75
 FT VARIANT 119 119
 FT VARIANT 128 128
 FT VARIANT 143 143
 FT CONFLICT 56 56
 FT
 SQ SEQUENCE 145 AA; 16073 MW; 6CA7CFA4574DD140 CRC64;

IRON (HEME DISTAL LIGAND).
 IRON (HEME PROXIMAL LIGAND).
 N -> S (IN A ALLELE).
 P -> A (IN A ALLELE).
 MK -> VQ (IN A ALLELE).
 N -> S (IN A ALLELE).
 D -> E (IN A ALLELE).
 K -> R (IN A ALLELE).
 N -> A (IN REF. 4; MAY BE DUE TO A
 DIFFERENCE IN BREED OF SHEEP).

Query Match 100.0%; Score 10; DB 1; Length 145;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10
 |||||
 DB 31 LVVYPTQRF 40

RESULT 18
 HBB_TRAST STANDARD; PRT; 145 AA.
 AC P04245;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 20-MAR-1987 (Rel. 04, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Tragelaphus strepsiceros (Greater kudu).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Tragelaphus.
 OX NCBI_TaxID=9946;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=85279893; PubMed=4026993;
 RA Rodewald K., Wiesner H., Braunitzer G.;
 RT "Primary structure of the hemoglobins from the greater kudu antelope
 RT (Tragelaphus strepsiceros).";
 RT Biol. Chem. Hoppe-Seyler 366:395-402(1985).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

DR PIR: A02391; HBBOKA.
 DR HSSP: P02070; 1HDA.
 DR InterPro: IPR002337; Beta.haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin.1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN.1.
 DR Heme: Oxygen transport; Transport; Erythrocyte;
 KM Polymorphism.
 FT METAL 62 62 IRON (HEME DISTAL LIGAND).
 FT METAL 91 91 IRON (HEME PROXIMAL LIGAND).
 FT VARIANT 15 15 G->S (IN A SECOND ALLELE).
 SQ SEQUENCE 145 AA: 16053 MW; EBOEF16E856E7522 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 145;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVPPWTFORF 10
 DB 31 LVVPPWTFORF 40

RESULT 19
 HBBI_IGUIG STANDARD; PRT; 146 AA.
 AC P18987;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DE 01-JUN-1994 (Rel. 29, Last annotation update)
 DE Hemoglobin beta-1 chain.
 GN HBBI.
 OS Iguana iguana (Common iguana).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Lepidodonta; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.
 OX NCBI_TaxID=8517;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=89207099; PubMed=3242545;
 RA Ruecknagel K.P., Braunitzer G., Wiesner H.;
 RT "Hemoglobins of reptiles. The primary structures of the alpha I- and
 RT beta I-chains of common iguana (Iguana iguana) hemoglobin.";
 RL Biol. Chem. Hoppe-Seyler 369:1143-1150(1988).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: S01665; HBIG1.
 DR HSSP: P02112; 1HBR.
 DR InterPro: IPR002337; Beta.haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin.1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN.1.
 KM Heme: Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA: 16111 MW; 097902EF83B05DA2 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVPPWTFORF 10
 DB 32 LVVPPWTFORF 41

RESULT 20
 HBBI_SPHPU

ID HBBI_SPHPU STANDARD; PRT; 146 AA.
 AC P10060;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta-1 chain.
 GN HBBI.
 OS Sphenodon punctatus (Hatteria) (Tuatara).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Lepidodonta; Rhynchocephalia; Sphenodontidae; Sphenodon.
 OX NCBI_TaxID=8508;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=89105321; PubMed=3214555;
 RA Abbasi A., Wells R.M.G., Brittain T., Braunitzer G.;
 RT "Primary structure of the hemoglobin from Sphenodon (Sphenodon
 RT punctatus, Tuatara, Rhynchocephalia). Evidence for the expression of
 RT alpha D-gene.";
 RL Biol. Chem. Hoppe-Seyler 369:755-764(1988).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: THERE ARE THREE FORMS OF HEMOGLOBIN IN SPHENODON: A, A',
 CC AND D. HB A IS A TETRAMER OF TWO ALPHA-A AND TWO BETA-1, HB A' IS
 CC A TETRAMER OF TWO ALPHA-A AND TWO BETA-2.
 CC -1- MISCELLANEOUS: SPHENODON'S HBS HAVE PROPERTIES NOT FOUND IN OTHER
 CC REPTILES: POOR COOPERATIVITY, HIGH AFFINITY FOR OXYGEN, SMALL BOHR
 CC AND HALLDANE EFFECTS, APPRECIABLE PHOSPHATE EFFECTS (THOSE
 CC PROPERTIES ARE ALSO FOUND IN THE HBS OF PRIMITIVE URODELE AND
 CC CAECILIAN AMPHIBIANS).
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: S01138; HB7J1.
 DR HSSP: P02118; 1AAE.
 DR InterPro: IPR002337; Beta.haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin.1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN.1.
 KM Heme: Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA: 16191 MW; E2714EE2794081DD CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVPPWTFORF 10
 DB 32 LVVPPWTFORF 41

RESULT 21
 HBBI_TAPPE STANDARD; PRT; 146 AA.
 AC P02064;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta-1 chain (Major).
 GN HBBI.
 OS Tapirus terrestris (Lowland tapir) (Brazilian tapir).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Euteria; Perissodactyla; Tapiridae; Tapirus.
 OX NCBI_TaxID=9801;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=85053021; PubMed=6149994;
 RA Mazur G., Braunitzer G.;
 RT "Perissodactyla: the primary structure of hemoglobins from the
 RT lowland tapir (Tapirus terrestris): glutamic acid in position 2 of
 RT the beta chains.";

RL Hoppe-Seyler's Z. Physiol. Chem. 365:1097-1106(1984).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: A02382; HBTPJ.
 DR HSP: P02062; 1HBE.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PRO0814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KM Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15973 MW; 1D53E28D108F6124 CEC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORF 10
 |||||
 DB 32 LVVYPWTORF 41

RESULT 22
 HB1_UROHA STANDARD; PRT: 146 AA.
 ID HB1_UROHA
 AC P18951.
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE Hemoglobin beta-1 chain (Fragments).
 OS Uromastix hardwicki (Indian spiny-tailed lizard).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Lepidodonta; Squamata; Iguania; Acrodonta; Agamidae; Uromastixinae;
 CC Uromastix.
 OX NCBI_TaxID=40250;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=84029159; PubMed=6628672;
 RA Nagyl S., Zaidi Z.H., von Bahr-Lindstroem H., Carlquist M.,
 RA Joernvall H.;
 RT "Characterization of hemoglobin from the lizard Uromastix
 RT hardwicki.";
 RT FEBS Lett. 167:290-295(1983).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: A05304; A05304.
 DR HSP: P02112; 1HBR.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PRO0814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KM Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 16136 MW; 3FPE0435F245EE9 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORF 10
 |||||
 DB 32 LVVYPWTORF 41

RESULT 23
 HB2_PANLE STANDARD; PRT: 146 AA.
 ID HB2_PANLE
 AC P18988;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta-2 chain.
 GN HB2.
 OS Panthera leo (Lion).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Panthera.
 OX NCBI_TaxID=9689;
 RN [1]
 RP SEQUENCE.
 RA Jahan M., Ahmed A., Braunitzer G., Zaidi Z.H., Goeltenboth R.;
 RT "Carnivora: the primary structures of adult lion (Panthera leo)
 RT hemoglobins.";
 RT Z. Naturforsch. C 42:1465-1470(1987).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: S03926; HBUL2.
 DR HSP: P02023; 1ABW.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PRO0814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KM Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15855 MW; AA82B6EBE6466BD CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORF 10
 |||||
 DB 32 LVVYPWTORF 41

RESULT 24
 HB2_TAPTE STANDARD; PRT: 146 AA.
 ID HB2_TAPTE
 AC P02065;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta-2 chain (Minor).
 GN HB2.
 OS Tapirus terrestris (lowland tapir) (Brazilian tapir).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Perissodactyla; Tapiridae; Tapirus.
 OX NCBI_TaxID=9801;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=85053021; PubMed=6149994;
 RA Mazur G., Braunitzer G.;
 RT "Perissodactyla: the primary structure of hemoglobins from the
 RT lowland tapir (Tapirus terrestris): glutamic acid in position 2 of
 RT the beta chains.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 365:1097-1106(1984).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.

CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR; A02383; HBBP.
 DR HSSP; P02062; 1BBE.
 DR InterPro: IPR002337; Beta.haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam; PF00042; globin; 1.
 DR PRINTS; PR00814; BETAHEM.
 DR PROSITE; PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SO SEQUENCE 146 AA; 16004 MM; DABE027FF554A271 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVYPTORF 10
 |||||
 Db 32 LVYPTORF 41

RESULT 25
 ID HBB_AILFU STANDARD: PRT; 146 AA.
 AC P18982;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Allurus fulgens (Lesser panda).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Procyonidae; Allurus.
 CX NCBI_Taxid=9649;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=87014854; PubMed=3762727;
 RA Tagle D.A., Miyamoto M.M., Goodman M., Hofmann O., Braunitzer G.,
 RA Goeltenboth R., Jalanka H.;
 RT "Hemoglobin of pandas: phylogenetic relationships of carnivores as
 RT ascertained with protein sequence data.";
 RL Naturwissenschaften 73:512-514(1986).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR; S06527; HBEOL.
 DR HSSP; P02023; 1BAB.
 DR InterPro: IPR002337; Beta.haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam; PF00042; globin; 1.
 DR PRINTS; PR00814; BETAHEM.
 DR PROSITE; PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SO SEQUENCE 146 AA; 15950 MM; B2082BB94462B2BB CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVYPTORF 10
 |||||
 Db 32 LVYPTORF 41

RESULT 26
 HBB_AILME

ID HBB_AILME STANDARD: PRT; 146 AA.
 AC P18983;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Alluropoda melanoleuca (Giant panda).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Alluropoda.
 CX NCBI_Taxid=9646;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=87014854; PubMed=3762727;
 RA Tagle D.A., Miyamoto M.M., Goodman M., Hofmann O., Braunitzer G.,
 RA Goeltenboth R., Jalanka H.;
 RT "Hemoglobin of pandas: phylogenetic relationships of carnivores as
 RT ascertained with protein sequence data.";
 RL Naturwissenschaften 73:512-514(1986).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR; S06529; HBEQG.
 DR HSSP; P02023; 1BAB.
 DR InterPro: IPR002337; Beta.haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam; PF00042; globin; 1.
 DR PRINTS; PR00814; BETAHEM.
 DR PROSITE; PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SO SEQUENCE 146 AA; 16021 MM; 796D36710867EA2 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVYPTORF 10
 |||||
 Db 32 LVYPTORF 41

RESULT 27
 ID HBB_ANTPA STANDARD: PRT; 146 AA.
 AC P1438;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Antrozous pallidus (Pallid bat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Chiroptera; Microchiroptera; Vespertilionidae;
 CC Antrozous.
 CX NCBI_Taxid=9440;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=88050104; PubMed=3675871;
 RA Kleinschmidt T., Koop B.F., Braunitzer G.;
 RT "The primary structure of the pallid bat (Antrozous pallidus,
 RT Chiroptera) hemoglobin.";
 RL Biol. Chem. Hoppe-Seyler 368:1197-1202(1987).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR; B29702; B29702.

DR HSSP; P02023; 1BAB.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
KM Heme; Oxygen transport; Transport; Erythrocyte.
FT METAL 63 63 IRON (HEME DISTAL LIGAND).
SO SEQUENCE 146 AA; 15898 MM; DB320D53704A60D6 CR64;

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTORF 10
| | | | | | | | | |
Db 32 LVVYPWTORF 41

RESULT 28
HBB_AOTTR 4 STANDARD; PRT; 146 AA.
ID HBB_AOTTR 4
AC P02035;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta chain.
GN HBB.
OS Aotus trivirgatus (Night monkey) (Douroucoulis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=9505;
RN [1]
RP SEQUENCE.
RX MEDLINE=72020149; PubMed=4999925;
RA Boyer S.H., Crosby E.F., Noyes A.N., Fuller G.F., Leslie S.E.,
RA Donaldson L.J., Vrablik G.R., Schaefer E.W. Jr., Thurmon T.F.;
RT "Primate hemoglobins: Some sequences and some proposals concerning
RT the character of evolution and mutation.";
RL Biochem. Genet. 5:405-448(1971).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: HETEROETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR HSSP; P02023; 1BAB.
DR PIR: A02356; HBKMN.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
KM Heme; Oxygen transport; Transport; Erythrocyte.
FT METAL 63 63 IRON (HEME DISTAL LIGAND).
SO SEQUENCE 146 AA; 15898 MM; B7025061FF5B5D98 CR64;

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTORF 10
| | | | | | | | | |
Db 32 LVVYPWTORF 41

RESULT 29
HBB_ATEGE STANDARD; PRT; 146 AA.
ID HBB_ATEGE
AC P02034;

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta chain.
GN HBB.
OS Ateles geoffroyi (Black-handed spider monkey),
OS Ateles paniscus (Black spider monkey), and
OS Ateles belzebuth (Long-haired spider monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Ateleinae; Ateles.
OX NCBI_TaxID=9509, 9510, 9507;
RN [1]
RP SEQUENCE.
RX SPECIES-A.geoffroyi, and A.belzebuth;
RX MEDLINE=72020149; PubMed=4999925;
RA Boyer S.H., Crosby E.F., Noyes A.N., Fuller G.F., Leslie S.E.,
RA Donaldson L.J., Vrablik G.R., Schaefer E.W. Jr., Thurmon T.F.;
RT "Primate hemoglobins: Some sequences and some proposals concerning
RT the character of evolution and mutation.";
RL Biochem. Genet. 5:405-448(1971).
RN [2]
RP SEQUENCE.
RC SPECIES-A.paniscus;
RX MEDLINE=70031568; PubMed=4981734;
RA Boyer S.H., Crosby E.F., Noyes A.N., Adams J.G.;
RT "The structure and biosynthesis of hemoglobins A and A2 in the new
RT world primate Ateles paniscus: a preliminary account.";
RL Ann. N.Y. Acad. Sci. 165:360-377(1969).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: HETEROETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR PIR: A02355; HBKMP.
DR PIR: B90233; HBKMK.
DR PIR: A90034; HBKMK.
DR HSSP; P02023; 1BAB.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
KM Heme; Oxygen transport; Transport; Erythrocyte.
FT METAL 63 63 IRON (HEME DISTAL LIGAND).
SO SEQUENCE 146 AA; 15913 MM; EDB309B8A214B095 CR64;

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTORF 10
| | | | | | | | | |
Db 32 LVVYPWTORF 41

RESULT 30
HBB_BALAC STANDARD; PRT; 146 AA.
ID HBB_BALAC
AC P18984;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta chain.
GN HBB.
OS Balaenoptera acutorostrata (Minke whale) (lesser rorqual).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
OC Balaenopteridae; Balaenoptera.
OX NCBI_TaxID=9767;
RN [1]
RP SEQUENCE.

RA Abbasi A., Rucknagel P., Matsuda G., Zaidi Z.H., Braunitzer G.;
 RT "The primary structure of Minke-whale (Balenoptera acutorostata -
 Cetacea) hemoglobin."
 RL J. Chem. Soc. Pak. 6:253-256(1984).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: S06521; HBWHK.
 DR HSSP: P02023; 1BAB.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin.1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN: 1.
 KW Heme: Oxygen transport; Transport; Erythrocyte;
 KW Polymorphism.
 KM METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 FT VARIANT 72 72 S -> A.
 FT VARIANT 87 87 T -> A.
 FT VARIANT 123 123 T -> L.
 FT VARIANT 128 128 A -> S.
 SQ SEQUENCE 146 AA; 16061 MW; C0AEB956165213B0 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPTQRF 10
 |||||
 Db 32 LVVYPTQRF 41

RESULT 31
 ID HBB_CALAR STANDARD; PRT; 146 AA.
 AC P18985;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Callithrix argentata (Black-tailed marmoset).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
 OC Callitrich.
 OX NCBI_TaxID=9482;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=84212383; PubMed=6427202;
 RA Malta T., Hayashida M., Matsuda G.;
 RT "Primary structures of adult hemoglobins of silvery marmoset,
 RT Callithrix argentatus, and cotton-headed tamarin, Saguinus oedipus."
 RL J. Biochem. 95:805-813(1984).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: S06513; HBCJB.
 DR HSSP: P02023; 1BAB.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin.1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN: 1.
 KW Heme: Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15952 MW; B3BDF9B6D1A18BA CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPTQRF 10
 |||||
 Db 32 LVVYPTQRF 41

RESULT 32
 ID HBB_CAVPO STANDARD; PRT; 146 AA.
 AC P02035;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=80114125; PubMed=527943;
 RA Braunitzer G., Schrank B., Stangl A., Wiesner H.;
 RT "Respiration at high altitudes, phosphate-protein interaction: the
 RT sequence of hemoglobins from guinea pig and dromedary."
 RL Hoppe-Seyler's Z. Physiol. Chem. 360:1941-1946(1979).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: A02411; HBGP.
 DR HSSP: P02067; 1QPW.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin.1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN: 1.
 KW Heme: Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15921 MW; E880DAC410019685 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPTQRF 10
 |||||
 Db 32 LVVYPTQRF 41

RESULT 33
 ID HBB_CEBAL STANDARD; PRT; 146 AA.
 AC P02040;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Cebus albifrons (White-fronted capuchin).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Cebus.
 OX NCBI_TaxID=9514;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=72076589; PubMed=5002362;
 RA Nure P.E., Sullivan B.;
 RT "Primate hemoglobins: their structure, function and evolution. I.
 RT Amino acid compositions of the tryptic peptides from the beta chain
 RT of Cebus albifrons.";
 RL Comp. Biochem. Physiol. 39B:797-814(1971).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: A02361; HBMQA.
 DR HSSP: P02023; 1DXT.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte;
 KW Polymorphism.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 FT VARIANT 13 13 A -> T (IN 50% OF THE CHAINS).
 SQ SEQUENCE 146 AA; 15959 MW; 1A8F8EC3BB6C51C0 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
 DB 32 LVVYPWTORE 41

RESULT 34
 HBB_CEBAP
 ID HBB_CEBAP STANDARD; PRT; 146 AA.
 AC P02041.
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Cebus apella (Brown-capped capuchin), and
 OS Cebus capucinus (White-faced sapsajou).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Cebus.
 OX NCBI_TaxID=9515, 9516;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=C.apella;
 RX MEDLINE=75042140; PubMed=4214886;
 RA Watanabe B.;
 RT "Amino acid sequences of the tryptic peptides from the beta chain of
 RT hemoglobin of tuffed capuchin monkey (Cebus apella).";
 RL Selkagaku 46:255-267(1974).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: B25477; B25477.
 DR HSSP: P02023; 1BAB.

DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15989 MW; 5B8F8ED3BA6020DC CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
 DB 32 LVVYPWTORE 41

RESULT 35
 HBB_CERAE
 ID HBB_CERAE STANDARD; PRT; 146 AA.
 AC P02028;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Cercopithecus aethiops (Green monkey) (Grivet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=9534;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=75040050; PubMed=4214754;
 RA Matsuda G., Maita T., Watanabe B., Araya A., Morokuma K., Goodman M.,
 RA Prychodko W.;
 RT "The amino acid sequences of the alpha and beta polypeptide chains of
 RT adult hemoglobin of the savannah monkey (Cercopithecus aethiops).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 354:1153-1155(1973).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: B02252; HBMG.
 DR HSSP: P02023; 1BAB.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15927 MW; 0FCD16DA69209CDE CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
 DB 32 LVVYPWTORE 41

RESULT 36
 HBB_CERSI
 ID HBB_CERSI STANDARD; PRT; 146 AA.
 AC P02066;

DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Ceratotherium simum (White rhinoceros) (Square-lipped rhinoceros).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium.
 OX NCBI_TaxID=9807;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=83055102; PubMed=7141412;
 RA Matur G., Braunltzer G., Wright P.G.;
 RT "The primary structure of the hemoglobin from a white rhinoceros
 (Ceratotherium simum, perissodactyla): beta 2 Glu.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 363:1077-1085(1982).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- MISCELLANEOUS: THE VARIANTS FOUND IN THIS SAMPLE FROM A SINGLE
 CC ANIMAL SUGGEST THE PRESENCE OF AT LEAST TWO BETA CHAIN LOCI.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: A02384; HBBRW.
 DR HSSP: P02062; IIBE.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin. 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte;
 GN Hemoglobin beta chain.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 FT VARIANT 62 62 A -> S.
 FT VARIANT 62 62 A -> T.
 FT VARIANT 116 116 K -> Q.
 OX SEQUENCE 146 AA; 15967 MW; E591654D27827FDC CRC64;
 SQ
 Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVVYPTQRF 10
 DB 32 LVVYPTQRF 41
 RESULT 37
 HBB_CERTO
 ID HBB_CERTO STANDARD; PRT; 146 AA.
 AC P02031;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=9531;
 RN [1]
 RP SEQUENCE.
 RA Cook C.N., Barnicot N.A.;
 RL Unpublished results, cited by:
 RL Yasunobu K.T., Tanaka M.;
 RL (In) Fasman G.D. (eds.);
 RL Handbook of biochemistry and molecular biology (3rd ed.),
 RL pp.3:441-460, CRC Press, Cleveland (1976).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.

CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: A04621; HBBKB.
 DR HSSP: P02023; IBAB.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin. 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte;
 GN Hemoglobin beta chain.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 OX SEQUENCE 146 AA; 15995 MW; 0ADE3525EDC06BB5 CRC64;
 SQ
 Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVVYPTQRF 10
 DB 32 LVVYPTQRF 41
 RESULT 38
 HBB_COLBA
 ID HBB_COLBA STANDARD; PRT; 146 AA.
 AC P02033;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Colobus badius (Red colobus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
 OC Colobus.
 OX NCBI_TaxID=9571;
 RN [1]
 RP SEQUENCE.
 RA Hewett-Emmett D., Barnicot N.A.;
 RL Unpublished results, cited by:
 RL Yasunobu K.T., Tanaka M.;
 RL (In) Fasman G.D. (eds.);
 RL Handbook of biochemistry and molecular biology (3rd ed.),
 RL pp.3:441-460, CRC Press, Cleveland (1976).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: B04620; HEMOB.
 DR HSSP: P02023; IBAB.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin. 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte;
 GN Hemoglobin beta chain.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 OX SEQUENCE 146 AA; 15870 MW; 314B6C810F76C9A CRC64;
 SQ

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RESULT 39
HBB_COLPO STANDARD: PRT: 146 AA.
AC P19885;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta chain.
CN HBB.
OS Colobus polykomos.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Colobus.
OX NCBI_TaxID=9572;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89342433; PubMed=2760921;
RA Vincent K.A., Wilson A.C.;
RT "Evolution and transcription of old world monkey globin genes."
RL J. Mol. Biol. 207:465-480(1989).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC -1- VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
CC -----
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CC or send an email to license@sdb.ch).
CC -----
DR EMBL: J00330; -; NOT ANNOTATED_CDS.
DR PIR: S04615; S04615.
DR HSSP: P02023; 1BAB.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport; Erythrocyte.
FT INTR_MET 0
FT METAL 63 IRON (HEME DISTAL LIGAND).
FT METAL 92 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 146 AA; 15853 MW; 4F7617B119B29C97 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
DB 32 LVVYPWTORE 41

RESULT 40
HBB_CROCR STANDARD: PRT: 146 AA.
AC P18986;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta chain.
CN HBB.
OS Crocuta crocuta (Spotted hyena).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Hyenidae; Crocuta.
OX NCBI_TaxID=9678;
RN [1]

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RP SEQUENCE.
RX MEDLINE=89302684; PubMed=2742752;
RA He C., Rodewald K., Braunitzer G., Goelenboth R.;
RT "Carnivora: primary structure of the hemoglobin from the spotted
RL hyena (Crocuta crocuta, Hyenidae).";
RL Biol. Chem. Hoppe-Seyler 370:417-423(1989).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC -1- VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR PIR: S04221; HBHS.
DR HSSP: P02023; 1BAB.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport; Erythrocyte.
FT METAL 63 IRON (HEME DISTAL LIGAND).
FT METAL 92 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 146 AA; 16017 MW; FC1994B6F07CC34 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
DB 32 LVVYPWTORE 41

RESULT 41
HBB_CTEGU STANDARD: PRT: 146 AA.
AC P20855;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta chain.
CN HBB.
OS Ctenodactylus gundi (Northern gundi).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Ctenodactylidae;
OC Ctenodactylus.
OX NCBI_TaxID=10166;
RN [1]
RP SEQUENCE.
RX MEDLINE=91197427; PubMed=2085415;
RA Beintema J.J., Rodewald K., Braunitzer G.;
RT "The primary structures of gundi (Ctenodactylus gundi, Rodentia)
RL hemoglobin and myoglobin.";
RL Biol. Chem. Hoppe-Seyler 371:1089-1099(1990).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC -1- VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR PIR: S13283; HBRTNG.
DR HSSP: P02067; 1OPW.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport; Erythrocyte.
FT METAL 63 IRON (HEME DISTAL LIGAND).
FT METAL 92 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 146 AA; 15846 MW; F3D582E685E182F8 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;

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Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTWQRF 10
DB 32 LVVYPTWQRF 41

RESULT 42

HBB_CYNBP STANDARD; PRT; 146 AA.

AC P11734;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta chain.
GN HBB.
OS Cynopterus sphinx (Indian short-nosed fruit bat).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;
OC Pteropodidae; Cynopterus.
OX NCBI_TaxID=9400;
RN [1]
RP MEDLINE=87299007; PubMed=3620110;
RX Sgouras J.G., Kleinschmidt T., Braunitzer G.;

RT "The primary structure of the hemoglobin of an Indian flying fox (Cynopterus sphinx, Megachiroptera).";
RL Biol. Chem. Hoppe-Seyler 368:675-680(1987).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT. FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR PIR: B29392; B29392.
DR HSSP: P02023; 1BAB.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin. 1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport; Erythrocyte.
FT METAL 63 63 IRON (HEME DISTAL LIGAND).
FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 146 AA; 15927 MW; 7BEC577E91F332AD CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTWQRF 10
DB 32 LVVYPTWQRF 41

RESULT 43

HBB_DASNO STANDARD; PRT; 146 AA.

AC P02087;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta chain.
GN HBB.
OS Dasypus novemcinctus (Nine-banded armadillo).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Edentata; Dasypodidae; Dasypus.
OX NCBI_TaxID=9361;
RN [1]
RP MEDLINE=81208315; PubMed=7236709;
RX de Jong W.W., Leunissen J.A.M., Cuijpers H.T.;

RT "Primary structure of the major beta-chain of armadillo (Dasypus novemcinctus) haemoglobin.";
RL Biochim. Biophys. Acta 668:57-62(1981).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR PIR: A02403; HBDN.
DR HSSP: P02023; 1BAB.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin. 1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport; Erythrocyte.
FT METAL 63 63 IRON (HEME DISTAL LIGAND).
FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 146 AA; 16326 MW; D57A75D7F08F5405 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTWQRF 10
DB 32 LVVYPTWQRF 41

RESULT 44

HBB_ECHTE STANDARD; PRT; 146 AA.

AC P24202;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta chain.
GN HBB.

OS Echinos telfairi (Lesser hedgehog tenrec).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Tenrecidae; Echinos.
OX NCBI_TaxID=9371;
RN [1]
RP MEDLINE=92172283; PubMed=1793518;
RX Piccinnini M., Kleinschmidt T., Gorr T., Weber R.E., Kuenzle H.,
RA Braunitzer G.;

RT "Primary structure and oxygen-binding properties of the hemoglobin from the lesser hedgehog tenrec (Echinos telfairi, Zamelodonta).";
RL Biol. Chem. Hoppe-Seyler 372:975-989(1991).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO DIFFERENT BETA CHAINS.
CC TWO EXTERNAL CYSTEINE RESIDUES AT BETA-16 AND BETA-52 CAUSE REVERSIBLE POLYMERIZATION TO OCTAMERS AND MOST LIKELY IRREVERSIBLE FORMATION OF HIGHER POLYMERS.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR PIR: S18398; S18398.
DR HSSP: P02023; 1BAB.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin. 1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport; Erythrocyte;
KW Polymorphism.

FT METAL 63 63 IRON (HEME DISTAL LIGAND).
FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
FT VARIANT 16 16 G -> C.
FT VARIANT 118 118 F -> L.

SQ SEQUENCE 146 AA; 16134 MW; 43FFAED7AD7EBC9D CFC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTWTF 10
Db 32 LVVYPTWTF 41

RESULT 45

HBH_EQUHE STANDARD; PRT; 146 AA.

AC P02063;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta chain.
GN HBB.
OS Equus hemionus kulan (Kulan) (Asiatic wild ass), and
OS Equus zebra (Mountain zebra).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=73334, 9791;

RN MEDLINE=82140509; PubMed=7061044;
RA Mazur G., Braunitzer G.;

RT "The sequence of hemoglobins from an asiatic wild ass and a mountain zebra."

RL Hope-Seyler's Z. Physiol. Chem. 363:59-71(1982).

CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.

CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.

CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.

CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

DR PIR; A02381; HBH0Z.

DR PIR; A91706; HBH0K.

DR HSSP; P02062; 1BB.

DR InterPro: IPR002337; Beta_haem.

DR InterPro: IPR000971; Globin.

DR Pfam: PF00042; globin. 1.

DR PRINTS: PR00814; BETAHAEM.

DR PROSITE: PS01033; GLOBIN; 1.

KW Heme; Oxygen transport; Transport; Erythrocyte.

FT METAL 63 63 IRON (HEME DISTAL LIGAND).

FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).

SQ SEQUENCE 146 AA; 16079 MW; 76BC3BCD2065498 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTWTF 10
Db 32 LVVYPTWTF 41

RESULT 46

HBH_ERIEU STANDARD; PRT; 146 AA.

AC P02059;
DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hemoglobin beta chain.

GN HBB.
OS Eulimnacus europaeus (Western European hedgehog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceus.

OX NCBI_TaxID=9365;

RN [1]

RP SEQUENCE.

RA MEDLINE=79109529; PubMed=762046;

RT "Amino acid sequences of the alpha and beta chains of adult hemoglobin of the European hedgehog, Erinaceus europaeus."

RT J. Biochem. 85:259-269(1979).

CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.

CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.

CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.

CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

DR PIR; A02377; HBH0H.

DR HSSP; P02067; 1QFW.

DR InterPro: IPR002337; Beta_haem.

DR InterPro: IPR000971; Globin.

DR Pfam: PF00042; globin. 1.

DR PRINTS: PR00814; BETAHAEM.

DR PROSITE: PS01033; GLOBIN; 1.

KW Heme; Oxygen transport; Transport; Erythrocyte.

FT METAL 63 63 IRON (HEME DISTAL LIGAND).

FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).

SQ SEQUENCE 146 AA; 15805 MW; 0E1520B8080DA2B CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTWTF 10
Db 32 LVVYPTWTF 41

RESULT 47

HBH_EULFU STANDARD; PRT; 146 AA.

AC P02053;
DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hemoglobin beta chain.

GN HBB.
OS Eulemur fulvus fulvus (Brown lemur).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Lemnidae; Eulemur.

OX NCBI_TaxID=40322;

RN [1]

RP SEQUENCE.

RA MEDLINE=79150872; PubMed=107155;

RT "Amino acid sequences of the alpha and beta chains of adult hemoglobin of the brown lemur, Lemur fulvus fulvus."

RT J. Biochem. 85:755-764(1979).

CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.

CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.

CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.

CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

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CC -----

DR EMBL: M15734; AAA36822.1; -

DR PIR: A02370; HBLER.

DR HSSP: P02023; 2HHE.

DR InterPro: IPR002337; Beta_haem.

DR InterPro: IPR000971; Globin.

DR Pfam: PF00042; globin. 1.

DR PRINTS: PR00814; BETAHAEM.

DR PROSITE: PS01033; GLOBIN; 1.

DR Heme: Oxygen transport; Erythrocyte.

FT INIT_MET 0

FT METAL 63 63 IRON (HEME DISTAL LIGAND).

FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).

SO SEQUENCE 146 AA; 15770 MW; 20D8B50B/D6FCEDD CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVYPTWTF 10
| | | | | | | | | |
DB 32 LVYPTWTF 41

RESULT 48

HBB_FELCA STANDARD; PRT; 146 AA.

ID HBB_FELCA STANDARD; PRT; 146 AA.

AC P07412;

DT 01-APR-1988 (Rel. 07, Created)

DT 01-APR-1988 (Rel. 07, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE Hemoglobin beta-A and beta-B chains.

GN HBB.

OS Felis silvestris catus (Cat).

OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

OX NCBI_TaxID=9685;

RN [1]

RP SEQUENCE.

RX MEDLINE-86050915; PubMed-4063071;

RA Abadzi A., Braundtzer G.;

RT "The primary structure of hemoglobins from the domestic cat (Felis

RT catus, Felidae)."

RL Biol. Chem. Hoppe-Seyler 366:699-704(1985).

CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE

CC VARIOUS PERIPHERAL TISSUES.

CC -1- SUBUNIT: HETEROETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.

CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.

CC -1- POLYMORPHISM: THERE ARE TWO ALLELES. THE SEQUENCE SHOWN IS THAT OF

CC BETA-A.

CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

CC PIR: B25203; B25203.

DR HSSP: P02067; IQPW.

DR InterPro: IPR002337; Beta_haem.

DR InterPro: IPR000971; Globin.

DR Pfam: PF00042; globin. 1.

DR PRINTS: PR00814; BETAHAEM.

DR PROSITE: PS01033; GLOBIN; 1.

DR Heme: Oxygen transport; Erythrocyte;

KW Polymorphism; Acetylation.

FT MOD_RES 1 1 ACETYLATION (IN BETA-B CHAIN).

FT METAL 63 63 IRON (HEME DISTAL LIGAND).

FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).

FT VARIANT 1 1 G -> S (IN BETA B).

FT VARIANT 4 4 T -> S (IN BETA B).

FT VARIANT 139 139 N -> S (IN BETA B).

FT VARIANT 144 144 K -> R (IN BETA B).

SO SEQUENCE 146 AA; 15926 MW; FB227B1E903CDABF CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVYPTWTF 10
| | | | | | | | | |
DB 32 LVYPTWTF 41

RESULT 49

HBB_GALCR STANDARD; PRT; 146 AA.

ID HBB_GALCR STANDARD; PRT; 146 AA.

AC P02050;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hemoglobin beta-1 and beta-2 chains.

GN HBB.

OS Galago crassicaudatus (Thick-tailed galago) (Otolenur crassicaudatus).

OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Strepsirhini; Galagonidae; Otolenur.

OX NCBI_TaxID=9463;

RN [1]

RP SEQUENCE.

RX MEDLINE-85225956; PubMed-4005042;

RA Matanabe B., Fujii T., Nakashima Y., Maeta T., Matsuda G.;

RT "Amino-acid sequences of the alpha and beta chains of adult

RT hemoglobins of the Grand Galago, Galago crassicaudatus.";

RL Biol. Chem. Hoppe-Seyler 366:265-269(1985).

CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE

CC VARIOUS PERIPHERAL TISSUES.

CC -1- SUBUNIT: HETEROETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.

CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.

CC -1- POLYMORPHISM: THERE ARE TWO ALLELES. THE SEQUENCE SHOWN IS THAT OF

CC BETA-1.

CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

DR PIR: A02367; HBGC2.

DR PIR: A90683; HBGC2.

DR HSSP: P02023; IBAB.

DR InterPro: IPR002337; Beta_haem.

DR InterPro: IPR000971; Globin.

DR Pfam: PF00042; globin. 1.

DR PRINTS: PR00814; BETAHAEM.

DR PROSITE: PS01033; GLOBIN; 1.

DR Heme: Oxygen transport; Erythrocyte;

KW Polymorphism.

FT METAL 63 63 IRON (HEME DISTAL LIGAND).

FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).

FT VARIANT 125 125 E -> Q (IN BETA-2).

SO SEQUENCE 146 AA; 15934 MW; FC2BBB1E091FACEE CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVYPTWTF 10
| | | | | | | | | |
DB 32 LVYPTWTF 41

RESULT 50

HBB_GORGO STANDARD; PRT; 146 AA.

ID HBB_GORGO STANDARD; PRT; 146 AA.

AC P02024;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hemoglobin beta chain.

GN HBB.

OS Gorilla gorilla gorilla (Lowland gorilla).

OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;

CC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE.
RA Zuckerkandl E.;
RL Submitted (JUL-1966) to the PIR data bank.
RN [2]
RP SEQUENCE OF 1-120 FROM N.A.
RX MEDLINE=92211718; PubMed=1556740;
RA Perrin-Peocant P., Gouy M., Nigou V.M., Trabuchet G.;
RT "Evolution of the primate beta-globin gene region: nucleotide
sequence of the delta-beta-globin intergenic region of gorilla and
phylogenetic relationships between African apes and man";
RL J. Mol. Evol. 34:17-30(1992).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

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or send an email to license@sib-sib.ch).

CC EMBL; X61109; CAA43421.1; .
DR PIR; S24304; HBGO.
DR HSSP; P02023; IBAB.
DR InterPro: IPR002337; Beta.haem.
DR InterPro: IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
KM Heme; Oxygen transport; Transport; Erythrocyte.
FT INIT MET 0 0
FT METAL 63 63 IRON (HEME DISTAL LIGAND).
FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 146 AA; 15839 MW; EACBDYCF8F33966A1 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10
DB 32 LVVYPTQRF 41

RESULT 51
HBB_HIPAM STANDARD; PRT; 146 AA.
AC P19016;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta chain.
GN HBB.
OS Hippopotamus amphibius (Hippopotamus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Cetartiodactyla; Hippopotamidae; Hippopotamus.
OX NCBI_TaxID=9833;
RN [1]
RP SEQUENCE.
RA Braunitzer G., Wright P.G., Stangl A., Schrank B., Krombach C.;
RT "Amino acid sequence of haemoglobin of hippopotamus (Hippopotamus
amphibius, Artiodactyla)";
RL S. Afr. J. Sci. 79:411-412(1983).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
VARIOUS PERIPHERAL TISSUES.

CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR HSSP; P02070; 1HDA.
DR InterPro: IPR002337; Beta.haem.
DR InterPro: IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
KM Heme; Oxygen transport; Transport; Erythrocyte.
FT METAL 63 63 IRON (HEME DISTAL LIGAND).
FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 146 AA; 16065 MW; 70315747EBDE6FE6 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10
DB 32 LVVYPTQRF 41

RESULT 52
HBB_HORSE STANDARD; PRT; 146 AA.
AC P02062;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta chain.
GN HBB.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE.
RX MEDLINE=81005583; PubMed=7409745;
RA Matsuda G., Maiba T., Braunitzer G., Schrank B.;
RT "Hemoglobins, XXXIII. Note on the sequence of the hemoglobins of the
horse";
RL Hoppe-Seyler's Z. Physiol. Chem. 361:1107-1116(1980).
RN [2]
RP SEQUENCE OF 1-82 AND 117-146.
RX MEDLINE=68397920; PubMed=4876811;
RA Smith D.B.;
RT "Amino acid sequences of some tryptic peptides from the beta-chain of
horse hemoglobin";
RL Can. J. Biochem. 46:825-843(1968).
RN [3]
RP DETERMINATION OF AMIDES, AND SEQUENCE OF 52-54.
RX MEDLINE=71027939; PubMed=5529282;
RA Smith D.B., Chung W.P.;
RT "Amide groups of some tryptic peptides from the beta-chain of horse
hemoglobin";
RL Can. J. Biochem. 48:1160-1164(1970).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=78007980; PubMed=561852;
RA Lader R.C., Heider E.J., Perutz M.F.;
RT "The structure of horse methaemoglobin at 2.0-A resolution";
RL J. Mol. Biol. 114:385-414(1977).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR PIR; A02380; HBHO.
DR PDB; 2DHB; 30-SEP-83.
DR PDB; 2MHB; 30-SEP-83.
DR PDB; 11BE; 23-DEC-96.

DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin. 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte;
 FT 3D-structure.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 FT HELIX 5 15
 FT TURN 16 17
 FT HELIX 20 34
 FT HELIX 36 45
 FT HELIX 51 55
 FT TURN 56 56
 FT HELIX 58 75
 FT TURN 76 77
 FT HELIX 78 84
 FT HELIX 86 93
 FT TURN 94 95
 FT TURN 100 100
 FT HELIX 101 121
 FT HELIX 124 142
 SO SEQUENCE 146 AA; 16008 MW; 734664793DA642EE CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10
 |||||
 Db 32 LVVYPTQRF 41

RESULT 53
 HBB_HUMAN STANDARD; PRT; 146 AA.
 AC P02023; Q14510; Q14481; Q13852; Q9UCP8; Q9UCP9;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Homo sapiens (Human),
 OS Pan troglodytes (Chimpanzee), and
 OS Pan paniscus (Pygmy chimpanzee) (Bonobo).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606, 9598, 9597;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Human;
 RA Braunltzer G., Gehring-Muller R., Hilschmann N., Hlase K., Hobom G.,
 RA Rudloff V., Wiltmann-Liebold B.;
 RT "The constitution of normal adult human haemoglobin.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 325:283-286(1961).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RX MEDLINE=81064667; PubMed=6254664;
 RA Lawn R.M., Efstratiadis A., O'Connell C., Maniatis T.;
 RT "The nucleotide sequence of the human beta-globin gene.";
 RL Cell 21:647-651(1980).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RX MEDLINE=77126403; PubMed=1019344;
 RA Marotta C., Forget B., Cohen-Solal M., Weissman S.M.;
 RT "Nucleotide sequence analysis of coding and noncoding regions of human
 beta-globin mRNA.";
 RL Prog. Nucleic Acid Res. Mol. Biol. 19:165-175(1976).
 RN [4]

RP SEQUENCE FROM N.A.
 RA Lu L., Hu Z.H., Du C.S., Fu Y.S.;
 RT "DNA sequence of the human beta-globin gene isolated from a healthy
 RT Chinese.";
 RL submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A., AND VARIANT DURHAM-N.C.
 RC TISSUE=Blood;
 RA Kutlar F., Abboud M., Leithner C., Holley L., Brisco J., Kutlar A.;
 RT "Electrophoretically silent, very unstable, thalassemic mutation at
 RT codon 114 of beta globin (hemoglobin Durham-N.C.) detected by cDNA
 RT sequencing of mRNA, from a Russian woman.";
 RL submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human; TISSUE=Skeletal muscle;
 RA Strausberg R.;
 RL submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A., AND VARIANT LOUISVILLE.
 RC TISSUE=Blood;
 RA Kutlar F., Harbin J., Brisco J., Kutlar A.;
 RT "Rapid detection of electrophoretically silent, unstable human
 RT hemoglobin 'Louisville', (Beta; Phe 42 Leu/Trp to Cys) by cDNA
 RT sequencing of mRNA.";
 RL submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE OF 121-146 FROM N.A.
 RC SPECIES=Human;
 RX MEDLINE=85205333; PubMed=2581851;
 RA Lang K.M., Spritz R.A.;
 RT "Cloning specific complete polyadenylated 3'-terminal cDNA
 RT segments.";
 RL Gene 33:191-196(1985).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF DEOXYHEMOGLOBIN.
 RC SPECIES=Human;
 RX MEDLINE=76027820; PubMed=1177322;
 RA Ferafi G.;
 RT "Three-dimensional fourier synthesis of human deoxyhaemoglobin at
 RT 2.5-A resolution: refinement of the atomic model.";
 RL J. Mol. Biol. 97:237-256(1975).
 RN [10]
 RP SEQUENCE.
 RC SPECIES=P. troglodytes;
 RX MEDLINE=66071496; PubMed=5855051;
 RA Rikfin D.B., Konigsberg W.;
 RT "The characterization of the tryptic peptides from the hemoglobin of
 RT the chimpanzee (Pan troglodytes).";
 RL Biochim. Biophys. Acta 104:457-461(1965).
 RN [11]
 RP SEQUENCE.
 RC SPECIES=P. paniscus;
 RX MEDLINE=83219265; PubMed=6406908;
 RA Goodman M., Braunltzer G., Stangl A., Schrank B.;
 RT "Evidence on human origins from haemoglobins of African apes.";
 RL Nature 303:546-548(1983).
 RN [12]
 RP HAPTOGLOBIN-BINDING.
 RC SPECIES=Human;
 RX MEDLINE=86242088; PubMed=3718478;
 RA Yoshioke N., Atassi M.Z.;
 RT "Haemoglobin binding with haptoglobin. Localization of the
 RT haptoglobin-binding sites on the beta-chain of human haemoglobin by
 RT synthetic overlapping peptides encompassing the entire chain.";
 RL Biochem. J. 234:453-456(1986).
 RN [13]
 RP GLYCATION IN N-TERMINUS.
 RC SPECIES=Human;
 RX MEDLINE=78138698; PubMed=6355569;
 RA Bunn H.F., Gabbay K.H., Gallop P.M.;
 RT "The glycosylation of hemoglobin: relevance to diabetes mellitus.";
 RL Science 200:21-27(1978).

RP [14] VARIANT ALABAMA.
 RX MEDLINE=75109326; PubMed=11157599;
 RA Brimhall B., Jones R.T., Schneider R.G., Hostly T.S., Tomlin G.,
 RA Atkins R.;
 RT "Two new hemoglobinbs. Hemoglobin Alabama (beta39(C5)Gln leads to Lys)
 RT and hemoglobin Montgomery (alpha 48(CD 6) Leu leads to Arg).";
 RL Blochim. Biophys. Acta 379:28-32(1975).
 RN [15]
 RP VARIANT ALESNA.
 RX MEDLINE=93321192; PubMed=8330974;
 RA Molchanova T.P., Postnikov Y.V., Pobedinskaya D.D., Smetanina N.S.,
 RA Moschen A.A., Kazanetz E.G., Tokarev Y.N., Huisman T.H.J.;
 RT "HB Alesna or alpha 2 beta 2 (2)67(ELI)Val-->Met: a new unstable
 RT hemoglobin variant identified through sequencing cf amplified DNA.";
 RL Hemoglobin 17:217-225(1993).
 RN [16]
 RP VARIANT J-ALTGEIDS GARDENS.
 RX MEDLINE=79067354; PubMed=721609;
 RA Adams J.G. III, Przywara K.P., Heller P., Shamsuddin M.;
 RT "Hemoglobin J Altgeld Gardens. A hemoglobin variant with a
 RT substitution of the proximal histidine of the beta-chain.";
 RL Hemoglobin 2:403-415(1978).
 RN [17]
 RP VARIANT ANKARAS.
 RX MEDLINE=74297498; PubMed=4850241;
 RA Arcasoy A., Casey R., Lehmann H., Cavdar A.O., Benki A.;
 RT "A new hemoglobin J from Turkey -- Hb Ankara (beta10 (A7) Ala-Asp).";
 RL FEBS Lett. 42:121-123(1974).
 RN [18]
 RP VARIANTS J-ANTAKYA AND COMPLUTENSE.
 RX MEDLINE=86216227; PubMed=3707965;
 RA Huisman T.H.J., Wilson J.B., Kutlar A., Yang K.-G., Chen S.-S.,
 RA Webber B.B., Altay C., Martinez A.V.;
 RT "HB J-Antakya or alpha 2 beta 2 (2)65(E9)Lys-->Met in a Turkish family
 RT and Hb complutense or alpha 2 beta 2 (2)127(H5)Gln-->Glu in a Spanish
 RT family: correction of a previously published identification.";
 RL Blochim. Biophys. Acta 871:229-231(1986).
 RN [19]
 RP VARIANT J-AUCKLAND.
 RX MEDLINE=88006903; PubMed=3654265;
 RA Williamson D., Wells R.M.G., Anderson R., Matthews J.;
 RT "A new unstable and low oxygen affinity hemoglobin variant: Hb J-
 RT Auckland [beta 25(B7)Gly-->Asp].";
 RL Hemoglobin 11:221-230(1987).
 RN [20]
 RP VARIANT AURORA.
 RX MEDLINE=96352910; PubMed=8718692;
 RA LaFetty J., Ali M., Matthew K., Eng B., Patterson M., Wayne J.S.;
 RT "Identification of a new high oxygen affinity hemoglobin variant: Hb
 RT Aurora [beta 139(H17) Asn-->Tyr].";
 RL Hemoglobin 19:335-341(1995).
 RN [21]
 RP VARIANT BREST.
 RX MEDLINE=88236755; PubMed=3384710;
 RA Baudin-Chich V., Wajzman H., Gombaud-Saintonge G., Arous N., Rlou J.,
 RA Briere J., Galacteros F.;
 RT "Hemoglobin Brest [beta 127 (H5)Gln-->Lys] a new unstable human
 RT hemoglobin variant located at the alpha 1 beta 1 interface with
 RT specific electrophoretic behavior.";
 RL Hemoglobin 12:179-188(1988).
 RN [22]
 RP VARIANT BRISBANE.
 RX MEDLINE=81239159; PubMed=6166590;
 RA Brennan S.O., Wells R.M., Smith H., Garrell R.W.;
 RT "Hemoglobin Brisbane: beta68 Leu replaced by His. A new high oxygen
 RT affinity variant.";
 RL Hemoglobin 5:325-335(1981).
 RN [23]
 RP VARIANT BUNBURY.
 RX MEDLINE=84031649; PubMed=6629823;
 RA Como P.F., Kennett D., Wilkinson T., Kronenberg H.;
 RT "A new hemoglobin with high oxygen affinity -- hemoglobin Bunbury:

RT	alpha 2 beta 2 [94 (FGI) Asp replaced by Asn].";
RL	Hemoglobin 7:413-421(1983).
RN	[24]
RP	VARIANT J-CAIRO.
RX	MEDLINE=76114933; PubMed=1247583;
RA	Garel M.-C., Hassan W., Coquelet M.T., Goossens M., Rosa J., Arous N.;
RT	"Hemoglobin J Cairo: beta 65 (E9) Lys leads to Gln, A new hemoglobin variant discovered in an Egyptian family.";
RL	Biochim. Biophys. Acta 420:97-104(1976).
RN	[25]
RP	VARIANT CAMPERDOWN.
RX	MEDLINE=75184109; PubMed=1138922;
RA	Wilkinson T., Chua C.G., Carrell R.W., Robin H., Exner T., Lee K.M.,
RT	Kroeneweg H.;
RT	"A new haemoglobin variant, haemoglobin Camperdown (beta 104 (G6)
RT	arginine->serine).";
RL	Biochim. Biophys. Acta 393:195-200(1975).
RN	[26]
QY	Query Match
DB	Best Local Similarity 100.0%; Score 10; DB 1; Length 146;
	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	1 LVVPPPTQRF 10
DV	32 LVVPPPTQRF 41
RESULT 54	
HB_HYLIA	STANDARD; PRT; 146 AA.
ID HB_HYLIA	P02025;
AC	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Hemoglobin beta chain.
GN	HB.
OS	Eukaryotes lar (Common gibbon).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX	NCBT_TaxID=9580;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=72020149; PubMed=4999925;
RA	Boyer S.H., Crosby E.F., Noyes A.N., Fuller G.F., Leslie S.E.,
RA	Donaldson L.J., Vrablik G.R., Schefer E.W. Jr., Thurmon T.F.;
RT	*Primate hemoglobins: Some sequences and some proposals concerning the character of evolution and mutation.*;
RL	Biochem. genet. 5:405-448(1971).
CC	- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.
CC	- SUBUNIT: HETEROQUATERNARY OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC	- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC	- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR	PIR; A02353; HBGI.
DR	HSSP; P02023; IBAI.
DR	InterPro; IPR002337; Beta_haem.
DR	InterPro; IPR0009371; Globin.
DR	Pfam; PF00042; globin; 1.
DR	PRINTS; PR00814; BETAHAE1.
DR	PROSITE; PS01033; GLOBIN; 1.
KW	Heme; Oxygen transport; Transport; Erythrocyte;
KW	Polymorphism.
KM	
FT	METAL 63 63 IRON (HEME DISTAL LIGAND).
FT	METAL 92 92 IRON (HEME PROXIMAL LIGAND).
FT	VARIANT 80 80 N -> D (IN COMMON ALLELE).
FT	VARIANT 87 87 Q -> K (IN COMMON AND UNCOMMON ALLELE).
SQ	SEQUENCE 146 AA; 15925 MW; EACBCT02CAD5B8D4 CRC64;
Query Match	100.0%; Score 10; DB 1; Length 146;
Best Local Similarity	100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

OY 1 LVVYPTQRF 10
 |||||
 DB 32 LVVYPTQRF 41

RESULT 55

HBB_LEMCA

ID HBB_LEMCA

STANDARD:

PRT: 146 AA.

AC P02054;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hemoglobin beta chain.

GN HBB.

OS Lemur catia (Ring-tailed lemur).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Strepsirrhini; Lemnidae; Lemur.

OX NCBI_TaxID=9447;

RN [1]

RP SEQUENCE.

RX MEDLINE=83185437; PubMed=6841124;

RA Copenhagen D.H., Dixon J.D., Duffy L.K.;

RT "Prosimian hemoglobins I. The primary structure of the beta-globin chain of Lemur catia."

RL Hemoglobin 7:1-14(1983).

CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.

CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.

CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.

CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

DR HSSP; P02023; 1BAB.

DR InterPro: IPR002337; Beta_haem.

DR InterPro: IPR000971; Globin.

DR Pfam: PF00042; globin; 1.

DR PRINTS: PR00814; BETAHEM.

DR PROSITE: PS01033; GLOBIN; 1.

DR Heme; Oxygen transport; Transport; Erythrocyte.

KW METAL 63 92 IRON (HEME DISTAL LIGAND).

FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).

SO SEQUENCE 146 AA; 15981 MM; EE1981B35D2B151 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10
 |||||
 DB 32 LVVYPTQRF 41

RESULT 56

HBB_LEMVA

ID HBB_LEMVA

STANDARD:

PRT: 146 AA.

AC P21667;

DT 01-MAY-1991 (Rel. 18, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hemoglobin beta chain.

GN HBB.

OS Lemur variegatus (Ruffed lemur) (Varecia variegata).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Strepsirrhini; Lemnidae; Varecia.

OX NCBI_TaxID=9455;

RN [1]

RP SEQUENCE.

RX Duffy L.K., Copenhagen D.H.;

RT "Prosimian hemoglobins II. Comparison of hemoglobin beta-chain primary structures in the genus Lemur."

RL (in) Schneck A.G., Paul C. (eds.);

RL Brussels hemoglobin symposium, pp.377-392, Editions de l'Universite de

RL Bruxelles, Brussels (1984).

CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.

CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.

CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.

CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

DR PIR; S06511; S06511.

DR HSSP; P02023; 1BAB.

DR InterPro: IPR002337; Beta_haem.

DR InterPro: IPR000971; Globin.

DR Pfam: PF00042; globin; 1.

DR PRINTS: PR00814; BETAHEM.

DR PROSITE: PS01033; GLOBIN; 1.

DR Heme; Oxygen transport; Transport; Erythrocyte.

FW METAL 63 63 IRON (HEME DISTAL LIGAND).

FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).

SO SEQUENCE 146 AA; 16124 MM; 3F2FA5BDFC4986BB CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10
 |||||
 DB 32 LVVYPTQRF 41

RESULT 57

HBB_LEPEU

ID HBB_LEPEU

STANDARD:

PRT: 146 AA.

AC P08535;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-AUG-1988 (Rel. 08, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hemoglobin beta chain.

GN HBB.

OS Lepus europaeus (European hare).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Lepus.

OX NCBI_TaxID=9983;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=87289065; PubMed=3615213;

RA Pauplin Y., Rech J.;

RT "Nucleotide sequence of hare adult beta-globin gene with flanking regions."

RL Nucleic Acids Res. 15:5899-5899(1987).

CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.

CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.

CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.

CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

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DR EMBL: Y00347; CAA68429.1; -

DR PIR: A27101; A27101.

DR HSSP; P02023; 1BAB.

DR InterPro: IPR002337; Beta_haem.

DR InterPro: IPR000971; Globin.

DR Pfam: PF00042; globin; 1.

DR PRINTS: PR00814; BETAHEM.

DR PROSITE: PS01033; GLOBIN; 1.

DR Heme; Oxygen transport; Transport; Erythrocyte.

FW INT_MET 0 0 IRON (HEME DISTAL LIGAND).

FT METAL 63 63 IRON (HEME DISTAL LIGAND).

FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 146 AA; 15931 MW; D9937E0F66281FDB CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10
DB 32 LVVYPTQRF 41

RESULT 58

HBH_LEPME STANDARD; PRT; 146 AA.
ID HBH_LEPME
AC P15166;
DT 01-APR-1990 (Rel. 14; Created)
DT 01-APR-1990 (Rel. 14; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Hemoglobin beta chain.
GN HBH.
OS Leptonychotes weddelli (Weddell seal).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Plimipedia; Phocidae; Leptonychotes.
OX NCBI_TaxId=9713;
RN [1]
RP SEQUENCE.
RX MEDLINE=89374816; PubMed=2775492;
RA Lin H.-X., Kleinschmidt T., Braunitzer G.;
RT "Carnivora: the primary structure of Weddell Seal (Leptonychotes
RT weddelli, plimipedia) hemoglobin.";
RL Biol. Chem. Hoppe-Seyler 370:707-713(1989).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR HSP: P02023; IBAH.
DR HSP: P02023; IBAH.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
DR Heme; Oxygen transport; Transport; Erythrocyte.
KM METAL 63 63 IRON (HEME DISTAL LIGAND).
FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 146 AA; 15993 MW; D3C8E6B61A52B0A1 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10
DB 32 LVVYPTQRF 41

RESULT 59

HBH_LORTA STANDARD; PRT; 146 AA.
ID HBH_LORTA
AC P02048;
DT 21-JUL-1986 (Rel. 01; Created)
DT 21-JUL-1986 (Rel. 01; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Hemoglobin beta chain.
GN HBH.
OS Loris tardigradus (Slender loris).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Loridae; Loris.
OX NCBI_TaxId=9468;

RN [1]
RP SEQUENCE.
RX MEDLINE=79027141; PubMed=100490;

RA Maita T., Goodman M., Matsuda G.;
RT "Amino acid sequences of the alpha and beta chains of adult
RT hemoglobin of the slender loris, Loris tardigradus.";
RL J. Biochem. 84:377-383(1978).

CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR HSP: P02023; IBAH.
DR HSP: P02023; IBAH.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
KM Heme; Oxygen transport; Transport; Erythrocyte.
FT METAL 63 63 IRON (HEME DISTAL LIGAND).
FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 146 AA; 15900 MW; 10E3CA7CC9580E22 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10
DB 32 LVVYPTQRF 41

RESULT 60

HBH_LUTLU STANDARD; PRT; 146 AA.
ID HBH_LUTLU
AC P10893;
DT 01-JUL-1989 (Rel. 11; Created)
DT 01-JUL-1989 (Rel. 11; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Hemoglobin beta chain.
GN HBH.
OS Lutra lutra (European river otter).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
OC Lutra.
OX NCBI_TaxId=9657;
RN [1]
RP SEQUENCE.
RX MEDLINE=89000194; PubMed=3166739;
RA Lin H.-X., Kleinschmidt T., Braunitzer G., Schell H.-G.;
RT "Carnivora: the primary structure of the common otter (Lutra lutra,
RT Mustelidae) hemoglobin.";
RL Biol. Chem. Hoppe-Seyler 369:349-355(1988).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR HSP: P02023; IBAH.
DR HSP: P02023; IBAH.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
KM Heme; Oxygen transport; Transport; Erythrocyte.
FT METAL 63 63 IRON (HEME DISTAL LIGAND).
FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 146 AA; 15950 MW; 174C272C1DAE36A6 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFORF 10
 |||||
 DB 32 LVVYPWTFORF 41

RESULT 61
 HBB_LYNLY STANDARD; PRT: 146 AA.
 AC P41328; 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Lynx lynx (European lynx).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Lynx.
 OX NCBI_TaxID=13125;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92384899; PubMed=1515033;
 RA Ahmed A., Jahan M., Braunitzer G.;
 RT "Carnivora: the primary structure of the major hemoglobin component
 from adult European lynx (Lynx lynx, Felidae).";
 RL J. Protein Chem. 11:39-43(1992).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: B53880; B53880.
 DR HSSP: P02067; 10PM.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM..
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63
 FT METAL 92
 FT METAL 92
 SQ SEQUENCE 146 AA; 15925 MW; 98C53C3FA32FB8F2 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFORF 10
 |||||
 DB 32 LVVYPWTFORF 41

RA Soskic V., Kleinschmidt T., Braunitzer G.;
 RT "The primary structure of the hemoglobin from the bat *Macrotus*
rt *californicus* (Chiroptera).";
 RL Biol. Chem. Hoppe-Seyler 368:199-204(1987).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: B26640; B26640.
 DR HSSP: P02023; 18AB.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM..
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63
 FT METAL 92
 FT METAL 92
 SQ SEQUENCE 146 AA; 16006 MW; F77CC19DCA08EE65 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFORF 10
 |||||
 DB 32 LVVYPWTFORF 41

RESULT 63
 HBB_MACFU STANDARD; PRT: 146 AA.
 AC P02027; 09TSL4; 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS *Macaca fuscata fuscata* (Japanese macaque),
 OS *Macaca fascicularis* (Crab eating macaque) (*Cynomolgus* monkey),
 OS *Macaca speciosa* (Stump-tail macaque), and
 OS *Macaca nemestrina* (Pig-tailed macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; *Macaca*.
 OX NCBI_TaxID=9543, 9541, 9553, 9545;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=M.fuscata;
 RX MEDLINE=72030553; PubMed=5000512;
 RA Matsuda G., Maeda T., Ota H., Tachikawa I., Tanaka Y., Araya A.,
 RA Nakashima Y.;
 RT "The primary structure of the beta-polypeptide chain of adult
 hemoglobin of the Japanese monkey (*Macaca fuscata fuscata*).";
 RL Int. J. Protein Res. 3:53-55(1971).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=M.fascicularis;
 RX MEDLINE=71108403; PubMed=5499429;
 RA Wade P.T., Barnicot N.A., Huehns E.R.;
 RT "Structural studies on the major and minor haemoglobin of the monkey
Macaca *irius*.";
 RL Biochim. Biophys. Acta 221:450-466(1970).
 RN [3]
 RP SEQUENCE OF 1-120 FROM N.A.
 RC SPECIES=M.fascicularis;
 RX MEDLINE=87254238; PubMed=3110424;
 RA Savatier P., Tribuchet G., Cheblioune Y., Faure C., Verdier G.,
 RA Nigon V.M.;
 RT "Nucleotide sequence of the beta-globin genes in gorilla and macaque:
 the origin of nucleotide polymorphisms in human.";

RL J. Mol. Evol. 24:309-318(1987).
 RN [4]
 RP SEQUENCE OF 106-146 FROM N.A.
 RC SPECIES-M.fascicularis; TISSUE-Blood;
 RX MEDLINE=20188801; PubMed=10723742;
 RA Francino M.P., Ochman H.;
 RT "Strand symmetry around the beta-globin origin of replication in
 RT primates.";
 RL Mol. Biol. Evol. 17:416-422(2000).
 RN [5]
 RP SEQUENCE.
 RC SPECIES-M.speciosa;
 RX MEDLINE=8631127; PubMed=4091973;
 RA Maier T., Tanaka Y., Nakayama S., Matsuda G.;
 RT "Amino acid sequences of the two major components of adult
 RT hemoglobins from the stump-tail monkey, Macaca speciosa.";
 RL Biol. Chem. Hoppe-Seyler 366:1149-1154(1985).
 RN [6]
 RP SEQUENCE.
 RC SPECIES-M.nemestrina;
 RX MEDLINE=87299001; PubMed=3304337;
 RA Kleinschmidt T., Sgouras J.G.;
 RT "Hemoglobin sequences.";
 RL Biol. Chem. Hoppe-Seyler 368:579-615(1987).
 RN [7]
 RP SEQUENCE.
 RC SPECIES-M.nemestrina;
 RX MEDLINE=7412665; PubMed=4206326;
 RA Nute P.E., Pataryas H.A.;
 RT "Amino acid compositions of the tryptic peptides comprising the beta-
 RT hemoglobin chain of Macaca nemestrina.";
 RL Am. J. Phys. Anthropol. 40:75-82(1974).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
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 CC -----
 DR EMBL: X05665; CAA29153.1; -
 DR EMBL: AF205410; AAF23761.1; -
 DR PIR: A02354; HBMOA.
 DR PIR: A04622; HBMOJ.
 DR PIR: A04623; HBMOQ.
 DR PIR: S10689; HBMDPM.
 DR PIR: C24693; C24693.
 DR HSSP: P02023; 1BAB.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin. 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN. 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT INIT MET 0
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SO SEQUENCE 146 AA; 15983 MW; 56ADCI559B20955B CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTFORF 10
 DB 32 LVVYPWTFORF 41

RESULT 64
 HBB_MACCG STANDARD; PRT; 146 AA.
 ID HBB_MACCG
 AC P24660;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Macrodonta gigas (Australian ghost bat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Megadermatidae;
 OC Macrodonta.
 OX NCBI_TaxID=9411;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92162193; PubMed=1789934;
 RA Singer G.A.M., Kleinschmidt T., Pettigrew J.D., Braunltzer G.;
 RT "The primary structure of the hemoglobin from the Australian ghost
 RT bat (Macrodonta gigas, Microchiroptera)."
 RL Biol. Chem. Hoppe-Seyler 372:1089-1095(1991).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- MISCELLANEOUS: GHOST BAT HAS TWO HEMOGLOBIN COMPONENTS IN THE
 CC RATIO 3:2. THEY SHARE IDENTICAL BETA-CHAINS AND DIFFER BY THREE
 CC REPLACEMENTS IN THE ALPHA CHAINS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: S20279; S20279.
 DR HSSP: P02023; 1BAB.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin. 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN. 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SO SEQUENCE 146 AA; 15926 MW; C44D93B82A1B4A69 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTFORF 10
 DB 32 LVVYPWTFORF 41

RESULT 65
 HBB_MANSF STANDARD; PRT; 146 AA.
 ID HBB_MANSF
 AC P08259;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Mandrillus sphinx (Mandrill) (Papio sphinx).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Mandrillus.
 OX NCBI_TaxID=9561;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=88293710; PubMed=3401326;
 RA Lin H.-X., Kleinschmidt T., Braunltzer G., Goltenboth R.;
 RT "The primary structure of the mandrill (Mandrillus sphinx, Primates)
 RT hemoglobin.";

RL Biol. Chem. Hoppe-Seyler 369:209-216(1988).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: S00540; HBBAM.
 DR HSP: P02023; IBAH.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15956 MW; 2CD5886C7D708046 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORF 10
 |||||
 DB 32 LVVYPWTORF 41

RESULT 66
 HBB_MARMA STANDARD; PRT; 146 AA.
 ID HBB_MARMA P08853;
 AC P08853;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Marmota marmota marmota (Alpine marmot).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
 OC Marmota.
 OX NCBI_TaxID=9994;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=86215569; PubMed=3707713;
 RA Sgouros J.G., Kleinschmidt T., Arnold W., Braunitzer G.;
 RT "The primary structure of the hemoglobin of the European marmot
 (Marmota marmota marmota, Rodentia).";
 RL Biol. Chem. Hoppe-Seyler 367:223-228(1986).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: B25729; B25729.
 DR HSP: P02067; IOPW.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15736 MW; 7DD33D1F41EB2B97 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 LVVYPWTORF 10
 |||||

DB 32 LVVYPWTORF 41

RESULT 67
 HBB_MEGLY STANDARD; PRT; 146 AA.
 ID HBB_MEGLY P1752;
 AC P1752;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Megaderma lyra (Indian false vampire).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Megadermatidae;
 OC Megaderma.
 OX NCBI_TaxID=9413;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=88163088; PubMed=3348887;
 RA Sgouros J.G., Kleinschmidt T., Braunitzer G.;
 RT "The primary structure of the hemoglobin of the Indian false vampire
 (Megaderma lyra, Microchiroptera).";
 RL Biol. Chem. Hoppe-Seyler 369:47-53(1988).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: S00341; HBBTV.
 DR HSP: P02023; IABW.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 16145 MW; AD822D938552470 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORF 10
 |||||
 DB 32 LVVYPWTORF 41

RESULT 68
 HBB_MELCA STANDARD; PRT; 146 AA.
 ID HBB_MELCA P15449;
 AC P15449;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Melivora capensis (Ratel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mellivorinae;
 OC Melivora.
 OX NCBI_TaxID=9664;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=89207098; PubMed=3242544;
 RA Rodewald K., Braunitzer G., Goeltenboth R.;
 RT "Carnivora: primary structure of the hemoglobins from ratel
 (Melivora capensis).";
 RL Biol. Chem. Hoppe-Seyler 369:1137-1142(1988).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE

CC VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR PIR; S01633; HBDR.
DR HSSP; P02023; 1BAB.
DR InterPro; IPR002337; Beta_haem.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport; Erythrocyte.
FT METAL 63 63 IRON (HEME DISTAL LIGAND).
FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 146 AA; 15948 MW; 866C273E1C83C999 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFQRF 10
Db 32 LVVYPWTFQRF 41
|||||

RESULT 69
HBB_MESAU STANDARD; PRT; 146 AA.
ID HBB_MESAU
AC P02094;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta-major chain.
GN HBB.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92223120; PubMed=1562610;
RA Lee K.M., Subar M., Li H., Boussios T.;
RT "Cloning of two adult hamster globin cDNAs (alpha and beta major).";
RL Blochm. Biophys. Acta 1130:343-344(1992).
RN [2]
RP SEQUENCE.
RA Braunitzer G., Schrank B., Stangl A., Wiesner H.;
RT "Respiration at high altitudes, phosphate-protein-interaction:
RT sequence of the hemoglobins of the hamster (Mesocricetus auratus) and
RT the camel (Camelus ferus, Camelidae).";
RL J. Chem. Soc. Pak. 2:1-7(1980).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X57030; CAA40346.1; -
DR PIR; A02410; HBHY.
DR HSSP; P02067; 1QPW.
DR InterPro; IPR002337; Beta_haem.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.

DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport; Erythrocyte.
FT INIT_MET 0 0
FT METAL 63 63 IRON (HEME DISTAL LIGAND).
FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
FT CONFLICT 50 52 SAS -> LPV (IN REF. 1).
FT CONFLICT 115 115 S -> I (IN REF. 1).
SQ SEQUENCE 146 AA; 15860 MW; FA4C582505A52C92 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFQRF 10
Db 32 LVVYPWTFQRF 41
|||||

RESULT 70
HBB_MUSLU STANDARD; PRT; 146 AA.
ID HBB_MUSLU
AC P23602;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta chain.
GN HBB.
OS Mustela lutreola (European mink).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Mustela.
OX NCBI_TaxID=9666;
RN [1]
RP SEQUENCE.
RX MEDLINE=90303485; PubMed=2363790;
RA Ahmed A., Jahan M., Braunitzer G.;
RT "Carnivora: the amino acid sequence of the adult European mink
RT (Mustela lutreola, Mustelidae) hemoglobins.";
RL Z. Naturforsch. C 45:223-228(1990).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR PIR; S10105; HBWNE.
DR HSSP; P02023; 1BAB.
DR InterPro; IPR002337; Beta_haem.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PRINTS; PR00814; BETAHAEM.
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport; Erythrocyte.
FT METAL 63 63 IRON (HEME DISTAL LIGAND).
FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 146 AA; 15935 MW; 046C273E1C83C98C CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTFQRF 10
Db 32 LVVYPWTFQRF 41
|||||

RESULT 71
HBB_MUSPF STANDARD; PRT; 146 AA.
ID HBB_MUSPF
AC P19017;
DT 01-NOV-1990 (Rel. 16, Created)

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DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta chain.
GN HBB
OS Muscula putorius furo (Ferret), and
OS Muscula putorius (European polecat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Muscula.
OX NCBI_TaxID=9669, 9668;
RN [1]
RP SEQUENCE.
RC SPECIES-M.p.furo;
RA Paulin Y., Hombrados I., Faure F., Han K.K., Neuzil E.;
RT "The primary structure of the beta-chain of the haemoglobins of the
RT ferret (Muscula putorius furo).";
RL Blochem. Soc. Trans. 16:608-609(1988).
RN [2]
RP SEQUENCE.
RC SPECIES-M.p.furo;
RA MEDLINE=90121748; PubMed=2610931;
RA Hombrados I., Vidal Y., Rodewald K., Braunitzer G., Neuzil E.;
RT "Carnivora: the primary structure of the alpha-chains of ferret
RT (Muscula putorius furo, Mustelidae) hemoglobins.";
RL Biol. Chem. Hoppe-Seyler 370:1133-1138(1989).
RN [3]
RP SEQUENCE.
RC SPECIES-M.putorius;
RA Ahmed A., Jahan M., Braunitzer G., Pechlaner H.;
RT "Carnivora: the amino acid sequence of the adult European polecat
RT (Muscula putorius, Mustelidae) hemoglobins.";
RL Z. Naturforsch. C 44:817-824(1989).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR PIR: S11534; HBMN.
DR PIR: S10103; HBKE.
DR HSSP: P02023; 1BAB.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin.1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN.1.
KW Heme: Oxygen transport; Transport; Erythrocyte.
FT METAL 63 63 IRON (HEME DISTAL LIGAND).
FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 146 AA; 15994 MW; DC99326ED2F4D8A4 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
DB 32 LVVYPWTORE 41

RESULT 72
HBB_MYOVE STANDARD: PRT: 146 AA.
AC P11758;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta chain.
GN HBB
OS Myotis veltfer (mouse-eared bat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Vespertilionidae;
OC Myotis.

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OX NCBI_TaxID=9435;
RN [1]
RP SEQUENCE.
RX MEDLINE=87157093; PubMed=3828074;
RA Kleinschmidt T., Koop B., Braunitzer G.;
RT "The primary structure of a mouse-eared bat (Myotis veltfer,
RT Chiroptera) hemoglobin.";
RL Biol. Chem. Hoppe-Seyler 367:1243-1249(1986).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR PIR: B25357; B25357.
DR HSSP: P02023; 1BAB.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin.1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN.1.
KW Heme: Oxygen transport; Transport; Erythrocyte.
FT METAL 63 63 IRON (HEME DISTAL LIGAND).
FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 146 AA; 15796 MW; 6BBD6EF2F929E840 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
DB 32 LVVYPWTORE 41

RESULT 73
HBB_NASNA STANDARD: PRT: 146 AA.
AC P26916;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta chain.
GN HBB
OS Nasua nasua (Ring-tailed coati).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Procyonidae; Nasua.
OX NCBI_TaxID=9651;
RN [1]
RP SEQUENCE.
RX MEDLINE=90253580; PubMed=2340073;
RA Ahmed A., Jahan M., Braunitzer G.;
RT "Carnivora: the primary structure of hemoglobin from adult coati
RT (Nasua nasua rufa, Procyonidae).";
RL J. Protein Chem. 9:23-29(1990).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR PIR: B39020; B39020.
DR HSSP: P02023; 1BAB.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin.1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN.1.
KW Heme: Oxygen transport; Transport; Erythrocyte.
FT METAL 63 63 IRON (HEME DISTAL LIGAND).
FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 146 AA; 16077 MW; E3FEC1B20657E457 CRC64;

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Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 |||||
 Db 32 LVVYPWTQRF 41

RESULT 74
 HBB_NYCCO STANDARD; PRT; 146 AA.
 AC P02049;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Nycticebus coucang (Slow loris).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Strepsirrhini; Loridae; Nycticebus.
 ON NCBI_TaxID=9470;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=74115165; PubMed=4782642;
 RA Matsuda G., Malta T., Watanabe B., Ota H., Araya A., Goodman M.,
 RA Pyschodro W.;
 RT "The primary structures of the alpha and beta polypeptide chains of
 RT adult hemoglobin of the slow loris (Nycticebus coucang).";
 RL Int. J. Pept. Protein Res. 5:419-421(1973).
 CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -!- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR; A02366; HBLS.
 DR HSSP; P02023; 1BAB.
 DR InterPro; IPR002337; Beta_haem.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PF00042; Globin; 1.
 DR PRINTS; PR00814; BETAHAEM.
 DR PROSITE; PS01033; GLOBIN; 1.
 KM Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15900 MW; FEE3CA7AE75A8026 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 |||||
 Db 32 LVVYPWTQRF 41

RESULT 75
 HBB_ODORO STANDARD; PRT; 146 AA.
 AC P10779;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Odobenus rosmarus divergens (Pacific walrus), and
 OS Arctocepalus galapagoensis (Galapagos fur seal).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Pinnipedia; Odobenidae; Odobenus.
 ON NCBI_TaxID=9708, 30584;
 RN [1]
 RP SEQUENCE.

RC SPECIES=O.r. divergens;
 RX MEDLINE=89207123; PubMed=2706084;
 RA Lin H.-X., Kleinschmidt T., Johnson M.L., Braunitzer G.;
 RT "Carlyora: the primary structure of the Pacific Walrus (Odobenus
 RT rosmarus divergens, Pinnipedia) hemoglobin.";
 RL Biol. Chem. Hoppe-Seyler 370:135-140(1989).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=A.galapagoensis;
 RX MEDLINE=92000163; PubMed=1910457;
 RA Jahan M., Ahmed A., Trillmich F., Braunitzer G.;
 RT "The complete primary structure of the marine Carnivora, galapagos
 RT fur seal (Arctocepalus galapagoensis, Otariidae) hemoglobins.";
 RL J. Protein Chem. 10:257-263(1991).
 CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -!- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR; S02820; HBW.
 DR PIR; B61434; B61434.
 DR HSSP; P02023; 1BAB.
 DR InterPro; IPR002337; Beta_haem.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PF00042; globin; 1.
 DR PRINTS; PR00814; BETAHAEM.
 DR PROSITE; PS01033; GLOBIN; 1.
 KM Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15920 MW; 866D62A06D59FDDC CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 |||||
 Db 32 LVVYPWTQRF 41

RESULT 76
 HBB_ONDZI STANDARD; PRT; 146 AA.
 ID HBB_ONDZI
 AC P02093;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Ondatra zibethicus (Muskrat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Arvicolinae;
 OC Ondatra.
 ON NCBI_TaxID=10060;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=84110063; PubMed=6363267;
 RA Bieber F.A., Braunitzer G.;
 RT "Primary structure of hemoglobins of the musk rat (Ondatra zibethica,
 RT Rodentia).";
 RL Hoppe-Seyler's Z. physiol. Chem. 364:1527-1536(1983).
 RN [2]
 RP REVISION TO 39.
 RX MEDLINE=87299001; PubMed=3304337;
 RA Bieber F.A., Braunitzer G.;
 RL Unpublished results, cited by:
 RL Kleinschmidt T., Sgouros J.G.;
 RL Biol. Chem. Hoppe-Seyler 368:579-615(1987).
 CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -!- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.

CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: A02409; HBOZ.
 DR HSSP: P02067; 10PW.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin.1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN.1.
 KW Heme: Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA: 15723 MW: 82136071CC4911F9 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORF 10
 |||||
 DB 32 LVVYPWTORF 41

RESULT 77
 HBB_ORNAN STANDARD; PRT; 146 AA.
 ID HBB_ORNAN
 AC P02111;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Ornithorhynchus anatinus (Duckbill platypus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
 OX NCBI_TaxId=9258;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76061123; PubMed=1191127;
 RA Whitaker R.G., Thompson E.O.P.;
 RT Studies on monotreme proteins. VI. Amino acid sequence of the beta-chain of haemoglobin from the platypus, Ornithorhynchus anatinus.";
 RL Aust. J. Biol. Sci. 28:353-365(1975).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: A02431; HBOZ.
 DR HSSP: P02023; 1BAB.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin.1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN.1.
 KW Heme: Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA: 15872 MW: E9043FEC82ADB2E1 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORF 10
 |||||
 DB 32 LVVYPWTORF 41

RESULT 78
 HBB_PAGLA

ID HBB_PAGLA STANDARD; PRT; 146 AA.
 AC P19646;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Paguma larvata (Masked palm civet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Viverridae; Paguma.
 OX NCBI_TaxId=9675;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=9116740; PubMed=2076197;
 RA He C., Braunltzer G., Goeltenboth R.;
 RT "Carnivora: the primary structure of hemoglobin from the Masked palm civet (Paguma larvata, Viverridae).";
 RL Biol. Chem. Hoppe-Seyler 371:1015-1020(1990).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: S13281; S13281.
 DR HSSP: P02023; 1BAB.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin.1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN.1.
 KW Heme: Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA: 16011 MW: FA51B7FB1B5675B CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORF 10
 |||||
 DB 32 LVVYPWTORF 41

RESULT 79
 HBB_PANPO STANDARD; PRT; 146 AA.
 ID HBB_PANPO
 AC P04244;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 20-MAR-1987 (Rel. 04, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Panthera pardus orientalis (Amur leopard).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Panthera.
 OX NCBI_TaxId=9692;
 RN [1]
 RP SEQUENCE.
 RA Abbasi A., Braunltzer G.;
 RT "The primary structure of haemoglobin from amur-leopard (Panthera pardus orientalis).";
 RL J. Protein Chem. 4:57-67(1985).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- MISCELLANEOUS: IN THE CAT FAMILY (FELIDAE), THE OXYGEN AFFINITY OF HEMOGLOBIN DEPENDS LITTLE OR NOT AT ALL ON THE ASSOCIATION WITH DIPHOSPHOGLYCERATE (DPG).
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: A02373; HBPB.

DR HSP; P02067; 10PW.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin. 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN. 1.
 DR Heme: Oxygen transport; Transport; Erythrocyte;
 Heme; Oxygen transport; Transport; Erythrocyte;
 Acetylation.
 FT MOD.RES 1 1 ACETYLATION.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15986 MW; FABI80FC94865 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
 |||||
 DB 32 LVVYPWTORE 41

RESULT 80
 HBB_PANTS
 ID HBB_PANTS STANDARD; PRT; 146 AA.
 AC P10584;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta-1 and beta-2 chains.
 GN HBB
 OS Panthera tigris sumatrae (Sumatran tiger),
 OS Panthera onca (Jaguar),
 OS Panthera leo (Lion), and
 OS Panthera pardus saxicolor (Northern persian leopard).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Panthera.
 NCBI_TaxID=9695, 9690, 9689, 9693;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=P.sumatrae;
 RA MEDLINE=89228545; PubMed=2713095;
 RA Jahan M.J., Ahmed A., Braunitzer G., Goltenboth R.;
 RT "Carnivora: the amino-acid sequence of the adult Sumatran tiger
 (Panthera tigris sumatrae) hemoglobins.";
 RL Biol. Chem. Hoppe-Seyler 370:27-33(1989).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=P.onca;
 RA MEDLINE=88107004; PubMed=3426807;
 RA Ahmed A., Jahan M., Zaidi Z.H., Braunitzer G., Goeltenboth R.;
 RT "The primary structure of the hemoglobins of the adult jaguar
 (Panthera onco. Carnivora).";
 RL Biol. Chem. Hoppe-Seyler 368:1385-1390(1987).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=P.leo;
 RA Jahan M., Ahmed A., Braunitzer G., Zaidi Z.H., Goeltenboth R.;
 RT "Carnivora: the primary structure of the major and minor hemoglobin
 components of adult north persian leopard (Panthera pardus
 saxicolor).";
 RL Z. Naturforsch. C 43:1341-1346(1988).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.

CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- MISCELLANEOUS: IN THE CAT FAMILY (FELIDAE), THE OXYGEN AFFINITY OF
 CC HEMOGLOBIN DEPENDS LITTLE OR NOT AT ALL ON THE ASSOCIATION WITH
 CC DIPOSPHOGLYCERATE (DPG).
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: S00522; HBJU.
 DR PIR: S02079; HBTXL.
 DR PIR: S11301; HBTXL.
 DR PIR: S03925; HBULL.
 DR PIR: S03928; HBPDLP.
 DR PIR: S03929; HBPDLP.
 DR HSP; P02067; 10PW.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin. 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN. 1.
 DR Heme: Oxygen transport; Transport; Erythrocyte;
 Heme; Oxygen transport; Transport; Erythrocyte;
 Acetylation.
 FT MOD.RES 1 1 ACETYLATION.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 FT VARIANT 1 1 S -> G (IN TIGER AND LEOPARD BETA-2).
 SQ SEQUENCE 146 AA; 15986 MW; A128EA70467D8D37 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
 |||||
 DB 32 LVVYPWTORE 41

RESULT 81
 HBB_PAPCY
 ID HBB_PAPCY STANDARD; PRT; 146 AA.
 AC P2030;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB
 OS Papio cynocephalus (Yellow baboon).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Papio.
 NCBI_TaxID=9556;
 RN [1]
 RP SEQUENCE.
 RC MEDLINE=80227364; PubMed=7390858;
 RA Nute P.E., Mahoney W.C.;
 RT "Complete primary structure of the beta chain from the hemoglobin of
 a baboon, Papio cynocephalus.";
 RL Hemoglobin 4:109-123(1980).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: A04624; HBBAY.
 DR HSP; P02023; IBAB.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin. 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN. 1.
 DR Heme: Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15895 MW; FOBBE0778BC9413 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPMWTF 10
 |||||
 DB 32 LVVYPMWTF 41

RESULT 82

HBB_PHYCA STANDARD; PRT; 146 AA.
 ID HBB_PHYCA
 AC P05909;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Phoca vitulina (Harbor seal).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Plinipedia; Phocidae; Phoca.
 OX NCBI_TaxID=9720;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=87157094; PubMed=3828075;
 RA Watanabe B., Maita T., Matsuda G., Goodman M., Johnson M.L.;
 RT "Antino-acid sequence of the alpha and beta chains of adult hemoglobin
 of the harbor seal, Phoca vitulina".
 RL Biol. Chem. Hoppe-Seyler 367:1251-1258(1986).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR HSSP; P02023; 1BAB.
 DR InterPro; IPR002337; Beta_haem.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PF00042; globin. 1.
 DR PRINTS; PR00814; BETAHAEM.
 DR PROSITE; PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 IRON (HEME PROXIMAL LIGAND).
 FT VARIANT 5 G -> A (IN BETA-1).
 FT VARIANT 11 L -> V (IN BETA-1).
 SQ SEQUENCE 146 AA; 15924 MW; 668D09A8A90A6749 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPMWTF 10
 |||||
 DB 32 LVVYPMWTF 41

RESULT 83

HBB_PHYCA STANDARD; PRT; 146 AA.
 ID HBB_PHYCA
 AC P05909;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta-I and beta-II chains.
 GN HBB.
 OS Physeter catodon (Sperm whale) (Physeter macrocephalus).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
 CC Physeteridae; Physeter.
 OX NCBI_TaxID=9755;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=86242695; PubMed=3718676;
 RA Abbasi A., Braunitzer G., Matsuda G., Maita T.;
 RT "The primary structure of sperm whale hemoglobin (Physeter catodon,
 cetacea)".
 RL Biol. Chem. Hoppe-Seyler 367:355-361(1986).

CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- POLYMORPHISM: THERE ARE TWO ALLELES. THE SEQUENCE SHOWN IS THAT OF
 CC BETA-II.

CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR; B25728; B25728.
 DR HSSP; P02023; 1BAB.
 DR InterPro; IPR002337; Beta_haem.
 DR InterPro; IPR000971; Globin.
 DR Pfam; PF00042; globin. 1.
 DR PRINTS; PR00814; BETAHAEM.
 DR PROSITE; PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte;
 KW Polymorphism.
 FT METAL 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 IRON (HEME PROXIMAL LIGAND).
 FT VARIANT 2 H -> Q (IN BETA-1).
 FT VARIANT 5 G -> A (IN BETA-1).
 FT VARIANT 11 L -> V (IN BETA-1).
 SQ SEQUENCE 146 AA; 16184 MW; 6C65A28ADEAEE656 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPMWTF 10
 |||||
 DB 32 LVVYPMWTF 41

RESULT 84

HBB_PIG STANDARD; PRT; 146 AA.
 ID HBB_PIG
 AC P02067; Q29025;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sharma A., Pearson C.T., Midha S., Okabe J., Yerie M., Pinton P.,
 RA Logan J., Kumar L.R.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE.
 RX MEDLINE=78170269; PubMed=565742;
 RA Braunitzer G., Schrank B., Stangl A., Schelthauer U.;
 RT "Hemoglobins. XVI. Sequence analysis of porcine hemoglobin.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 359:137-146(1978).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RX MEDLINE=95082021; PubMed=7990139;
 RA Katz D.S., White S.P., Huang W., Kumar R., Christianson D.W.;
 RT "Structure determination of aquomet porcine hemoglobin at 2.8-A
 resolution".
 RL J. Mol. Biol. 244:541-553(1994).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
 RX MEDLINE=20180433; PubMed=10713517;
 RA Lu T.-H., Panneerselvam K., Llaw Y.-C., Kan P., Lee C.-J.;

RT "Structure determination of porcine haemoglobin.";
 RL Acta Crystallogr. D 56:304-312(2000).
 CC - FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC - SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC - TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC - SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 CC -----
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 CC -----
 DR EMBL: X86791; CAN60490.1; -
 DR PIR: A02385; HBPB.
 DR PDB: 2PGH; 30-NOV-94.
 DR PDB: 1QPM; 04-JUN-99.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte;
 KW 3D-structure.
 FT INIT_MER 0
 FT METAL 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 IRON (HEME PROXIMAL LIGAND).
 FT CONFLICT 125 N -> D (IN REF. 2).
 SQ SEQUENCE 146 AA; 16034 MW; B542033A32FDDC93 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
 |||||
 DB 32 LVVYPWTQRF 41

RESULT 85
 HBB_PREEN STANDARD; PRT; 146 AA.
 AC P02032;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Presbytis entellus (Human langur).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
 OC Presbytis.
 OX NCBI_TaxID=9574;
 RN [1]
 RP SEQUENCE.
 RA Matsuda G., Malta T., Nakashima Y., Barnabas J., Ranjekar P.K.,
 RA Gandhi N.S.;
 RT "The primary structures of the alpha and beta polypeptide chains of
 RT adult hemoglobin of the Hanuman langur (Presbytis entellus).";
 RL Int. J. Pept. Protein Res. 5:423-425(1973).
 CC - FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC - SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC - TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC - SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: B02250; HBMP.
 DR HSSP: P02023; IBAB.
 DR InterPro: IPR002337; Beta_haem.

DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15985 MW; 4F7608A555C1EDD2 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
 |||||
 DB 32 LVVYPWTQRF 41

RESULT 86
 HBB_PROCR STANDARD; PRT; 146 AA.
 AC P23020;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Proteles cristatus (Aardwolf).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Hyainidae; Proteles.
 OX NCBI_TaxID=9680;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=92000305; PubMed=1910578;
 RA Stoeva S., Kleinschmidt T., Braunitzer G., Scheil H.-G.;
 RT "The primary structure of the hemoglobin from the aardwolf (Proteles
 RT cristatus, Hyainidae)."; 372:393-399(1991).
 RL Biol. Chem. Hoppe-Seyler 372:393-399(1991).
 CC - FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC - SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC - TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC - SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: S16110; S16110.
 DR HSSP: P02023; IBAB.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15987 MW; E94D81F73B129834 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTQRF 10
 |||||
 DB 32 LVVYPWTQRF 41

RESULT 87
 HBB_PROHA STANDARD; PRT; 146 AA.
 AC P02086;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hemoglobin beta chain.
 GN HBB.
 OS Procavia capensis habessinica (Abyssinian hyrax).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Hyracoidea; Procaviidae; Procavia.
 CC NCBI_TaxID=9814;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=84030514; PubMed=6629339;
 RA Kleinschmidt T., Braunitzer G.;
 RT "The primary structure of hemoglobin of the rock hyrax (Procavia
 habessinica, Hyracoidea): insertion of glutamine in the alpha
 chains.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:1303-1313(1983).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: A02402; HBHR.
 DR HSSP: P02023; 1BAB.
 DR InterPro: IPR0002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PRO0814; BETAHEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte; Acetylation.
 FT MOD_RES 1 63 ACETYLATION (IN 20% OF THE CHAINS).
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 FT SEQUENCE 146 AA; 16205 MW; 1045076010D8EC1 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10
 |||||
 DB 32 LVVYPTQRF 41

RESULT 88
 HBB_PROLO STANDARD; PRT; 146 AA.
 AC P18989;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Procyon lotor (Raccoon).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Procyonidae; Procyon.
 CC NCBI_TaxID=9654;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=79026831; PubMed=701090;
 RA Brimhall B., Stangland K., Jones R.T., Becker R.R., Bailey T.J.;
 RT "Amino acid sequence of the hemoglobin of raccoon (Procyon lotor).";
 RL Hemoglobin 2:351-370(1978).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: S06523; HBRR.
 DR HSSP: P02023; 1BAB.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PRO0814; BETAHEM.
 DR PROSITE: PS01033; GLOBIN; 1.

KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 FT SEQUENCE 146 AA; 16007 MW; ACEBDBFF141941 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10
 |||||
 DB 32 LVVYPTQRF 41

RESULT 89
 HBB_PTEAL STANDARD; PRT; 146 AA.
 ID HBB_PTEAL
 AC P14391;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Pteropus alecto (Black flying fox).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;
 CC Pteropodidae; Pteropus.
 CC NCBI_TaxID=9402;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=8914963; PubMed=3228493;
 RA Kleinschmidt T., Sgouros J.G., Pettigrew J.D., Braunitzer G.;
 RT "The primary structure of the hemoglobin from the grey-headed flying
 fox (Pteropus poliocephalus) and the black flying fox (P. alecto,
 Megachiroptera).";
 RL Biol. Chem. Hoppe-Seyler 369:975-984(1988).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: S01309; HBFXB.
 DR HSSP: P02023; 1BAB.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PRO0814; BETAHEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte;
 KW Polymorphism.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 FT VARIANT 139 139 N -> T
 FT SEQUENCE 146 AA; 15937 MW; FC0590DF3543643 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPTQRF 10
 |||||
 DB 32 LVVYPTQRF 41

RESULT 90
 HBB_PTEBR STANDARD; PRT; 146 AA.
 ID HBB_PTEBR
 AC P10836;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

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DE Hemoglobin beta chain.
GN HBB.
OS Pteronura brasiliensis (Giant otter), and
OS Martes foina (Beach marten).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
OC Pteronura.
OX NCBI_TaxID=9672, 9659;
RN [1]
RP SEQUENCE.
RC SPECIES-P. brasiliensis;
RX MEDLINE=89228546; PubMed=2713096;
RA Kleinschmidt T., Braunitzer G., Scheil H.-G.;
RT "Carnivora: the primary structure of the giant otter (Pteronura
RT brasiliensis, Mustelidae) hemoglobin.";
RL Biol. Chem. Hoppe-Seyler 370:35-40(1989).
RN [2]
RP SEQUENCE.
RC SPECIES-M. foina;
RX MEDLINE=90359058; PubMed=2390216;
RA Ruecknagel K.P., Wiesner H., Braunitzer G.;
RT "Carnivora: the primary structure of the beach marten (Martes foina,
RT Mustelidae) hemoglobin.";
RL Biol. Chem. Hoppe-Seyler 371:503-509(1990).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR PIR: S02081; HBOTG.
DR PIR: S10599; HBBDM.
DR HSSP: P02023; IBAH.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin. 1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN. 1.
KW Heme; Oxygen transport; Transport; Erythrocyte.
FT METAL 63 63 IRON (HEME DISTAL LIGAND).
FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 146 AA; 15934 MW; 4DAC273AC7A08CBE CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
DB 32 LVVYPWTORE 41

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RL Biol. Chem. Hoppe-Seyler 369:975-984(1988).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR PIR: S01311; HBFXG.
DR HSSP: P02023; IBAH.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin. 1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN. 1.
KW Heme; Oxygen transport; Transport; Erythrocyte;
KW Polymorphism.
FT METAL 63 63 IRON (HEME DISTAL LIGAND).
FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
FT VARIANT 139 139 N -> Y.
SQ SEQUENCE 146 AA; 15947 MW; FEF8BFDCA843570 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPWTORE 10
DB 32 LVVYPWTORE 41

RESULT 92
HBB_RABIT
ID HBB_RABIT STANDARD; PRT; 146 AA.
AC P02057;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta-1 and beta-2 chains.
GN HBB1 AND HBB2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE (BETA-1).
RX MEDLINE=69219353; PubMed=5789874;
RA Best J.S., Flamm U., Braunitzer G.;
RT "Haemoglobins, XVII. The primary structure of the beta-chain of
RT rabbit haemoglobin.";
RL Hoppe-Seyler S. Z. Physiol. Chem. 350:563-580(1969).
RN [2]
RP SEQUENCE FROM N.A. (BETA-1).
RX MEDLINE=80014491; PubMed=482942;
RA van Ooyen A., van den Berg J., Mantel N., Weissmann C.;
RT "Comparison of total sequence of a cloned rabbit beta-globin gene and
RT its flanking regions with a homologous mouse sequence.";
RL Science 206:337-344(1979).
RN [3]
RP SEQUENCE FROM N.A. (BETA-1).
RX MEDLINE=77183599; PubMed=558827;
RA Estratiadis A., Kafatos F.C., Maniatis T.;
RT "The primary structure of rabbit beta-globin mRNA as determined from
RT cloned DNA.";
RL Cell 10:571-585(1977).
RN [4]
RP SEQUENCE FROM N.A. (BETA-1).
RX MEDLINE=78237860; PubMed=277327;
RA Sim G.K., Estratiadis A., Jones C.W., Kafatos F.C., Koehler M.,
RA Kronenberg H.M., Maniatis T., Regier J.C., Roberts B.F., Rosenthal N.;
RT "Studies on the structure of genes expressed during development.";
RL Cold Spring Harb. Symp. Quant. Biol. 42:933-945(1978).
RN [5]
RP SEQUENCE OF 1-61 FROM N.A. (BETA-1).

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RA MEDLINE=80132479; PubMed=7357610;
 RA Pavlakis G.N., Lockard R.E., Yamvakopoulos N., Rieser L.,
 RA Rajbhandary U.L., Yournakis J.N.;
 RT "Secondary structure of mouse and rabbit alpha- and beta-globin
 RT mRNAs: differential accessibility of alpha and beta initiator AUG
 RT codons towards nucleases.";
 RL Cell 19:91-102(1980).
 [6]
 RP OCCURRENCE AND FREQUENCY OF ALLELIC CHAINS.
 RX MEDLINE=75053122; PubMed=4530669;
 RA Garrick M.D., Hafner R., Bricker J., Garrick L.M.;
 RT "Genetic variation in the primary structure of the beta chain of
 RT rabbit hemoglobin.";
 RL Ann. N.Y. Acad. Sci. 241:436-438(1974).
 [7]
 RP SEQUENCE FROM N.A. (BETA-2).
 RX MEDLINE=80090069; PubMed=519769;
 RA Hardison R.C., Butler E.T. III, Lacy E., Maniatis T., Rosenthal N.,
 RA Efstratiadis A.;
 RT "The structure and transcription of four linked rabbit beta-like
 RT globin genes.";
 RL Cell 18:1285-1297(1979).
 [8]
 RP SEQUENCE FROM N.A. (BETA-2).
 RX MEDLINE=89178632; PubMed=2486295;
 RA Margot J.B., Demers G.W., Hardison R.C.;
 RT "Complete nucleotide sequence of the rabbit beta-like globin gene
 RT cluster. Analysis of intergenic sequences and comparison with the
 RT human beta-like globin gene cluster.";
 RL J. Mol. Biol. 205:15-40(1989).
 [9]
 RP SEQUENCE OF 99-114 FROM N.A. (BETA-1).
 RX MEDLINE=79114395; PubMed=264241;
 RA van den Berg J., van Ooyen A., Mantel N., Schamboom A., Grosveld G.,
 RA Flavell R.A., Weissmann C.;
 RT "Comparison of cloned rabbit and mouse beta-globin genes showing
 RT strong evolutionary divergence of two homologous pairs of introns.";
 RL Nature 276:37-44(1978).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- POLYMORPHISM: THERE ARE TWO ALLELES. THE SEQUENCE SHOWN IS THAT OF
 CC BETA-1; THE MOST FREQUENT OF THE TWO COMMON ALLELES.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 CC -----
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 CC -----
 CC
 DR EMBL: J00660; AAA31274.1; -
 DR EMBL: V00862; CAA24251.1; -
 DR EMBL: M18818; AAA02985.1; -
 DR EMBL: V00878; CAA24247.1; -
 DR EMBL: V00879; CAA24248.1; -
 DR EMBL: M10843; AAA31270.1; -
 DR EMBL: K03256; AAA31268.1; -
 DR EMBL: M10831; AAA31271.1; -
 DR EMBL: J00659; AAA31273.1; -
 DR EMBL: M10833; AAA31272.1; -
 DR EMBL: M10832; AAA31272.1; JOINED.
 DR PIR: A02375; HBRB.
 DR PIR: S03090; S03090.
 DR HSSP: P02023; 1BAB.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAE.
 DR PRINTS: PR00814; BETAHAE.

DR PROSITE: PS01033; GLOBIN. 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte;
 KW Polymorphism.
 FT INT_MET 0 0
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 FT VARIANT 52 52 N -> H (IN BETA 2).
 FT VARIANT 56 56 N -> S (IN BETA 2).
 FT VARIANT 76 76 S -> N (IN BETA 2).
 FT VARIANT 112 112 I -> V (IN BETA 2).
 SQ SEQUENCE 146 AA; 16001 MW; 88CD6D3D0E8251D1 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LVVYPTQRF 10
 DB 32 LVVYPTQRF 41
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 |||||

RESULT 93
 HBB_RH1UN STANDARD; PRT; 146 AA.
 ID HBB_RH1UN
 AC P0907;
 DT 01-MAR-1989 (Rel. 10. Created)
 DT 01-MAR-1989 (Rel. 10. Last sequence update)
 DT 16-OCT-2001 (Rel. 40. Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS Rhinoceros unicornis (Greater Indian rhinoceros).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Rhinoceros.
 OX NCBI_TaxID=9809;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=87271129; PubMed=3606819;
 RA Abbas A., Weber R.E., Braunitzer G., Gollentz R.;
 RT "Molecular basis for ATP/2,3-bisphosphoglycerate control switch-over
 RT (poliklotherm/homeotherm) an intermediate amino-acid sequence in the
 RT hemoglobin of the great Indian rhinoceros (Rhinoceros unicornis,
 RT perissodactyla)." ;
 RL Biol. Chem. Hoppe-Seyler 368:323-332(1987).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: B26543; B26543.
 DR HSSP: P02062; 1HBE.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00814; BETAHAE.
 DR PROSITE: PS01033; GLOBIN. 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15857 MW; 09D6907DE4BFF15 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPTQRF 10
 DB 32 LVVYPTQRF 41
 |||||
 |||||

RESULT 94
 HBB_RH0UAE

ID HBB_RQDAE STANDARD: PRT: 146 AA.
AC P02058;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta chain.
GN HBB.
OS Roussetus aegyptiacus (Egyptian roussette) (Egyptian fruit bat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;
OC Pteropodidae; Roussetus.
OX NCBI_TaxID=9407;
RN [1]
RP SEQUENCE.
RA MEDLINE=83055089; PubMed=7141404;
RA Kleinschmidt T., Braunitzer G.;
RT "Primary structure of the hemoglobins from the Egyptian fruit bat
RT (Roussetus aegyptiacus, Chiroptera).";
RL Hoppe-Seyler's Z. Physiol. Chem. 363:1209-1215(1982).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC PIR: A02376; HBTF.
DR HSSP: P02023; 1BAB.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
GN Heme; Oxygen transport; Transport; Erythrocyte.
FT METAL 63 63 IRON (HEME DISTAL LIGAND).
FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 146 AA; 15955 MW; E1C5946CFE060DB7 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPMPTQRF 10
| | | | | | | | | |
DB 32 LVVYPMPTQRF 41

RESULT 95
HBB_SAGFU STANDARD: PRT: 146 AA.
AC P02039;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta chain.
GN HBB.
OS Saginus fuscicollis (Brown-headed tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saginus.
OX NCBI_TaxID=9487;
RN [1]
RP SEQUENCE.
RA MEDLINE=77021459; PubMed=823937;
RA Lin K.D., Kim Y.K., Chernoff A.L.;
RT "Primary structure of the marmoset (Saguinus fuscicollis) hemoglobin.
RT I. Use of tryptic maleylated peptides in the solubilization and
RT sequence elucidation of the alpha- and beta-chains.";
RL Biochem. Genet. 14:427-440(1976).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC PIR: A02360; HBMOF.

DR HSSP: P02023; 1BAB.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
GN Heme; Oxygen transport; Transport; Erythrocyte.
FT METAL 63 63 IRON (HEME DISTAL LIGAND).
FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 146 AA; 15914 MW; 22CED35A842C7D20 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPMPTQRF 10
| | | | | | | | | |
DB 32 LVVYPMPTQRF 41

RESULT 96
HBB_SAGMY STANDARD: PRT: 146 AA.
AC P02038;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hemoglobin beta chain.
GN HBB.
OS Saginus mystax (Moustached tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saginus.
OX NCBI_TaxID=9488;
RN [1]
RP SEQUENCE.
RA MEDLINE=72020149; PubMed=4999925;
RA Boyer S.H., Crosby E.F., Noyes A.N., Fuller G.F., Leslie S.E.,
RA Donaldson L.J., Vrablik G.R., Schaefer E.W. Jr., Thurmon T.F.;
RT "Primate hemoglobins: Some sequences and some proposals concerning
RT the character of evolution and mutation.";
RL Biochem. Genet. 5:405-448(1971).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC PIR: A02359; HBMM.
DR HSSP: P02023; 1BAB.
DR InterPro: IPR002337; Beta_haem.
DR InterPro: IPR000971; Globin.
DR Pfam: PF00042; globin; 1.
DR PRINTS: PR00814; BETAHAEM.
DR PROSITE: PS01033; GLOBIN; 1.
GN Heme; Oxygen transport; Transport; Erythrocyte.
FT METAL 63 63 IRON (HEME DISTAL LIGAND).
FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 146 AA; 15958 MW; 57EAB8B694579C93 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVYPMPTQRF 10
| | | | | | | | | |
DB 32 LVVYPMPTQRF 41

RESULT 97
HBB_SAGNI STANDARD: PRT: 146 AA.
AC P02037;

DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS *Saguinus nigricollis* (Black-and-red tamarin), and
 OS *Saguinus oedipus* (cotton-top tamarin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
 NCBI_TaxID=9489, 9490;
 RN [1]
 RP SEQUENCE.
 RC SPECIES-S.nigricollis;
 RX MEDLINE=72020149; PubMed=4999925;
 RA Boyer S.H., Crosby E.F., Noyes A.N., Fuller G.F., Leslie S.E.,
 RA Donaldson L.J., Vrablik G.R., Schaefer E.W. Jr., Thurmon T.F.;
 RT "Primate hemoglobins: Some sequences and some proposals concerning
 RT the character of evolution and mutation.";
 RL Biochem. Genet. 5:405-448(1971).
 RN [2]
 RP SEQUENCE.
 RC SPECIES-S.oedipus;
 RX MEDLINE=84212383; PubMed=6427202;
 RA Malta T., Hayashida M., Matsuda G.;
 RT "Primary structures of adult hemoglobins of silvery marmoset,
 RT *Callithrix argentatus*, and cotton-headed tamarin, *Saguinus oedipus*.";
 RL J. Biochem. 95:805-813(1984).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: A02358; HBMON.
 DR PIR: D28865; D28865.
 DR HSSP: P02023; 1BAB.
 DR InterPro: IPR002337; Beta.haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin.1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN: 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15972 MW; B7FEDAC380078992 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. NO. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPMWQRF 10
 |||||
 DB 32 LVVYPMWQRF 41

RESULT 98
 ID HBB_SAISC STANDARD; PRT; 146 AA.
 AC P02036;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS *Saimiri sciureus* (Common squirrel monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
 NCBI_TaxID=9521;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72020149; PubMed=4999925;
 RA Boyer S.H., Crosby E.F., Noyes A.N., Fuller G.F., Leslie S.E.,
 RA Donaldson L.J., Vrablik G.R., Schaefer E.W. Jr., Thurmon T.F.;

RT "Primate hemoglobins: Some sequences and some proposals concerning
 RT the character of evolution and mutation.";
 RL Biochem. Genet. 5:405-448(1971).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: A02357; HBMON.
 DR HSSP: P02023; 1BAB.
 DR InterPro: IPR002337; Beta.haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin.1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN: 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte;
 KW Polymorphism.
 FT METAL 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 IRON (HEME PROXIMAL LIGAND).
 FT VARIANT 76 A -> T (IN ALLELIC SEQUENCE).
 SQ SEQUENCE 146 AA; 15912 MW; 5343151FEE31DDCD CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. NO. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPMWQRF 10
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 DB 32 LVVYPMWQRF 41

RESULT 99
 ID HBB_SPAEH STANDARD; PRT; 146 AA.
 AC P02090;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS *Spalax leucodon ehrenbergi* (Ehrenberg's mole rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Spalacinae;
 OC Spalax.
 NCBI_TaxID=30637;
 RN [1]
 RP SEQUENCE (KARYOTYPE 2N=60).
 RX MEDLINE=84287390; PubMed=6469215;
 RA Kleinschmidt T., Nevo E., Braunitzer G.;
 RT "The primary structure of the hemoglobin of the mole rat (*Spalax
 RT ehrenbergi*, rodentia, chromosome species 60).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 365:531-537(1984).
 RN [2]
 RP SEQUENCE (KARYOTYPE 2N=52).
 RX MEDLINE=86000133; PubMed=4041241;
 RA Kleinschmidt T., Nevo E., Goodman M., Braunitzer G.;
 RT "Mole rat hemoglobin: primary structure and evolutionary aspects in a
 RT second karyotype of *Spalax ehrenbergi*, Rodentia, (2n = 52).";
 RL Biol. Chem. Hoppe-Seyler 366:679-685(1985).
 CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: A02406; HBOL.
 DR HSSP: P02067; 1QPM.
 DR InterPro: IPR002337; Beta.haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin.1.
 DR PRINTS: PR00814; BETAHAEM.
 DR PROSITE: PS01033; GLOBIN: 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.

FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15784 MW; EDE5043E5275154A CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 |||
 DB 32 LVVYPWTQRF 41

RESULT 100
 HBB_SPECI
 ID HBB_SPECI STANDARD; PRT; 146 AA.
 AC P09421;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemoglobin beta chain.
 GN HBB.
 OS *Spermophilus citellus* (European suslik) (*Citellus citellus*).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Scurinae;
 OC *Spermophilus*.
 OX NCBI_TaxID=9997;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=87128535; PubMed=3814354;
 RA Soskic V., Grujic-Injac B., Braunttzer G.;
 RT "The primary structure of the hemoglobin of the European Souslik
 (*Citellus citellus*, Rodentia)." ;
 RL Biol. Chem. Hoppe-Seyler 367:1159-1166(1986).
 CC -!- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
 CC VARIOUS PERIPHERAL TISSUES.
 CC -!- SUBUNIT: HETEROOTETRAMER OF TWO ALPHA CHAINS AND TWO BETA CHAINS.
 CC -!- TISSUE SPECIFICITY: RED BLOOD CELLS.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR HSSP; B25359; B25359.
 DR PIR; B25359; B25359.
 DR InterPro: IPR002337; Beta_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam; PF00042; globin_1.
 DR PRINTS; PR00814; BETAHAEM.
 DR PROSITE; PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 63 63 IRON (HEME DISTAL LIGAND).
 FT METAL 92 92 IRON (HEME PROXIMAL LIGAND).
 SQ SEQUENCE 146 AA; 15759 MW; 93C40CA2D1418A94 CRC64;

Query Match 100.0%; Score 10; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 4.2e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVYPWTQRF 10
 |||
 DB 32 LVVYPWTQRF 41

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 Job time: 217 sec

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L13 ANSWER 1 OF 6 MEDLINE
 AN 1999350023 MEDLINE
 DN 99350023 PubMed ID: 10423160
 TI Antirheumatic agents and leukocyte recruitment. New light on the mechanism of action of oxaceprol.
 AU Parnham M J
 CS Pharmacological Institute for the Life Sciences, J.W. Goethe University, Frankfurt am Main, Germany.. michael.parnham@pliva.hr
 SO BIOCHEMICAL PHARMACOLOGY, (1999 Jul 15) 58 (2) 209-15. Ref: 61
 Journal code: 9Z4; 0101032. ISSN: 0006-2952.
 CY ENGLAND: United Kingdom
 DT Journal; Article; (JOURNAL ARTICLE)
 General Review; (REVIEW)
 (REVIEW, TUTORIAL)
 LA English
 FS Priority Journals
 EM 199908
 ED Entered STN: 19990816
 Last Updated on STN: 19990816
 Entered Medline: 19990805
 AB Most anti-inflammatory agents used in the treatment of joint diseases exert inhibitory effects on leukocyte infiltration. Methotrexate, a disease-modifying drug, and corticosteroids also inhibit leukocyte accumulation during inflammation. However, the mechanisms of action of these different compounds on leukocytes vary and in the case of non-steroidal anti-inflammatory drugs (NSAIDs) the mechanism(s) may be indirect. No current drug for inflammatory or degenerative joint disease has been proposed to act specifically by an inhibitory action on neutrophilic leukocytes. Oxaceprol is an amino acid derivative that has been used for several years for the treatment of osteoarthritis and rheumatoid arthritis, ameliorating pain and stiffness and showing good gastrointestinal safety, particularly in comparison with NSAIDs. Recent experimental studies have shown that oxaceprol does not inhibit the synthesis of prostaglandins in vitro, but markedly inhibits neutrophil infiltration into the joints of rats with adjuvant arthritis. These results support earlier screening data showing inhibition by oxaceprol of leukocyte infiltration into sites of acute inflammation. In studies on surgical ischemia reperfusion in hamsters in vivo, oxaceprol was an effective inhibitor of leukocyte adhesion and extravasation. It is proposed that oxaceprol represents a therapeutic agent for degenerative and **inflammatory joint diseases**, which acts predominantly by **inhibiting leukocyte adhesion and migration**.

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L2 ANSWER 1 OF 1 MEDLINE
 AN 96062323 MEDLINE
 DN 96062323 PubMed ID: 7594507
 TI An **important role** for the **chemokine**
macrophage inflammatory protein-1 alpha in the pathogenesis of the
 T cell-mediated autoimmune disease, experimental autoimmune
 encephalomyelitis.
 AU Karpus W J; Lukacs N W; McRae B L; Strieter R M; Kunkel S L; Miller S D
 CS Department of Microbiology and Immunology, Northwestern University
 Medical School, Chicago, IL 60611, USA.
 NC AI35934 (NIAID)
 HL50057 (NHLBI)
 NS34510 (NINDS)
 +
 SO JOURNAL OF IMMUNOLOGY, (1995 Nov 15) 155 (10) 5003-10.
 Journal code: IFB; 2985117R. ISSN: 0022-1767.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Abridged Index Medicus Journals; Priority Journals
 EM 199512
 ED Entered STN: 19960124
 Last Updated on STN: 20000303
 Entered Medline: 19951218
 AB Experimental autoimmune encephalomyelitis (EAE) is a CD4+ T
 cell-mediated,
 inflammatory demyelinating disease of the central nervous system (CNS)
 that serves as a model for the human demyelinating disease, multiple
 sclerosis. A critical event in the pathogenesis of EAE is the entry of
 both Ag-specific T lymphocytes and Ag-nonspecific mononuclear cells into
 the CNS. In the present report we investigated the role of two C-C
 chemokines (macrophage inflammatory protein-1 alpha (MIP-1 alpha) and
 monocyte chemotactic protein-1) and a C-x-C chemokine (MIP-2) in the
 pathogenesis of EAE. Production in the CNS of MIP-1 alpha, but not that
 of
 MIP-2, a rodent homologue of IL-8, or monocyte chemotactic protein-1,
 correlated with development of severe clinical disease. Administration of
 anti-MIP-1 alpha, but not that of anti-monocyte chemotactic protein-1,
 prevented the development of both acute and relapsing paralytic disease
 as
 well as infiltration of mononuclear cells into the CNS initiated by the
 transfer of neuroantigen peptide-activated T cells. Ab therapy could also
 be used to ameliorate the severity of ongoing clinical disease.
 Anti-MIP-1
 alpha did not affect the activation of encephalitogenic T cells as
 measured by cytokine secretion, surface marker expression, and ability to
 adoptively transfer EAE. These results demonstrate that MIP-1 alpha plays
 an important role in directing the chemoattraction of mononuclear
 inflammatory cells in the T cell-mediated autoimmune disease, EAE.

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L3 ANSWER 1 OF 1 MEDLINE
 AN 93231454 MEDLINE
 DN 93231454 PubMed ID: 8472896
 TI **Astrocyte expression of mRNA encoding cytokines IP-10 and JE/MCP-1 in experimental autoimmune encephalomyelitis.**
 AU Ransohoff R M; Hamilton T A; Tani M; Stoler M H; Shick H E; Major J A; Estes M L; Thomas D M; Tuohy V K
 CS Research Institute, Cleveland Clinic Foundation, Ohio 44195.
 NC HL29582 (NHLBI)
 NS 29095 (NINDS)
 NSK08-01265 (NINDS)
 +
 SO FASEB JOURNAL, (1993 Apr 1) 7 (6) 592-600.
 Journal code: FAS; 8804484. ISSN: 0892-6638.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 EM 199305
 ED Entered STN: 19930604
 Last Updated on STN: 20000303
 Entered Medline: 19930518
 AB Mononuclear leukocytes preferentially accumulate in the central nervous system (CNS) during the course of experimental autoimmune encephalomyelitis (EAE). To address factors that govern leukocyte trafficking in EAE, we monitored expression of mRNAs encoding IP-10 and JE/MCP-1, which are members of a family of chemoattractant cytokines. A transient burst of IP-10 and JE/MCP-1 mRNA accumulation in the CNS occurred, in close relation to the onset of histologic and clinical disease. In situ hybridizations showed, unexpectedly, that astrocytes were the major source of mRNAs encoding IP-10 and JE/MCP-1. These observations implicate astrocyte-derived cytokines as potential chemoattractants for inflammatory cells during EAE.

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L6 ANSWER 1 OF 1 MEDLINE
 AN 95332927 MEDLINE
 DN 95332927 PubMed ID: 7608739
 TI **Macrophage inflammatory protein-1 alpha** in the
 cerebrospinal fluid of patients with **multiple sclerosis**
 and **other inflammatory neurological**
diseases.
 AU Miyagishi R; Kikuchi S; Fukazawa T; Tashiro K
 CS Department of Neurology, Hokkaido University School of Medicine, Sapporo,
 Japan.
 SO JOURNAL OF THE NEUROLOGICAL SCIENCES, (1995 Apr) 129 (2) 223-7.
 Journal code: JBJ; 0375403. ISSN: 0022-510X.
 CY Netherlands
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 EM 199508
 ED Entered STN: 19950828
 Last Updated on STN: 19950828
 Entered Medline: 19950815
 AB The level of **macrophage inflammatory protein-1 alpha**
 (MIP-1 alpha), a newly discovered cytokine of chemokine family, was
 determined in cerebrospinal fluid (CSF) from 18 patients with
multiple sclerosis (MS) and from control patients with
 other neurological disorders by an enzyme-linked immunosorbent assay
 (ELISA). The concentration of MIP-1 alpha in CSF was significantly
 elevated in MS in relapse (4.4 pg/ml) compared with non-inflammatory
 neurological disease control samples (0.3 pg/ml) ($p < 0.0002$). These
 concentrations in MS patients correlated well with leukocyte cell counts
 and protein content in CSF ($r = 0.845$, $p < 0.0001$; $r = 0.853$, $p < 0.0001$,
 respectively). In other inflammatory neurological disorders such as
 Behcet's disease and HTLV-1 associated myelopathy, significantly
 increased
 CSF levels of MIP-1 alpha were also observed. Chemokines are reported to
 play an important role in an early event of inflammation such as
 lymphocyte traffic. This report is the first study which confirmed the
 involvement of a chemokine in MS and other inflammatory neurological
 disorders.

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L2 ANSWER 1 OF 6 MEDLINE
AN 97323420 MEDLINE
DN 97323420 PubMed ID: 9179868
TI Investigation of inhibition angiotensin-converting enzyme (ACE) activity and **opioid** activity of two hemorphins, LVV-hemorphin-5 and VV-hemorphin-5, isolated from a defined peptic hydrolysate of **bovine hemoglobin**.
AU Zhao Q; Piot J M
CS Laboratoire de Genie proteique et cellulaire, Pole Sciences et Technologies, Universite de La Rochelle, France... qzhao@bio.univ-lr.fr
SO NEUROPEPTIDES, (1997 Apr) 31 (2) 147-53.
Journal code: 8103156. ISSN: 0143-4179.
CY SCOTLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199708
ED Entered STN: 19970902
Last Updated on STN: 19970902
Entered Medline: 19970818
AB Two peptides, LVV-hemorphin-5 and VV-hemorphin-5, were isolated from a defined peptic **bovine hemoglobin** hydrolysate by reversed-phase HPLC. These peptides were identified as 31-38 and 32-38 fragments of **beta chain of bovine hemoglobin**. Their inhibitory activity towards angiotensin-converting enzyme and **opioid** potency were determined. Since their amino acid sequences show close homology with spinorphin, which is found in human cerebrospinal fluid and in the bovine spinal cord, the possible physiological role in vivo of these peptides was discussed.

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L2 ANSWER 2 OF 6 MEDLINE
 AN 95319594 MEDLINE
 DN 95319594 PubMed ID: 7596489
 TI VV-hemorphin-7 and LVV-hemorphin-7 released during in vitro peptic hemoglobin hydrolysis are morphinomimetic peptides.
 AU Garreau I; Zhao Q; Pejoan C; Cupo A; Piot J M
 CS Laboratoire de Genie Proteique et Cellulaire, Pole Sciences et Techniques,
 La Rochelle, France.
 SO NEUROPEPTIDES, (1995 Apr) 28 (4) 243-50.
 Journal code: 8103156. ISSN: 0143-4179.
 CY SCOTLAND: United Kingdom
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 EM 199508
 ED Entered STN: 19950817
 Last Updated on STN: 20000303
 Entered Medline: 19950803
 AB Two **opioid** peptides were generated by in vitro pepsin treatment of **bovine hemoglobin**. These peptides were identified using a GPI test and purified using HPLC chromatographic techniques. They correspond to fragments 31-40 (LVV-hemorphin-7) and 32-40 (VV-hemorphin-7) of the **beta-chain** of **bovine hemoglobin**. Binding experiments strongly confirm that VV-hemorphin-7 and LVV-hemorphin-7 are **opioid** peptides since they inhibited [3H]naloxone binding to rat brain membranes. Our results indicate that VV-hemorphin-7 and LVV-hemorphin-7 exhibit a lesser potency both in GPI and binding tests. Selectivity and affinity of these purified peptides and synthetic hemorphin-7 for opioid receptors is discussed.

2 type?
 Neuropeptides 95

mw
 delta opioid antagonist.

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L2 ANSWER 5 OF 6 MEDLINE
 AN 93080543 MEDLINE
 DN 93080543 PubMed ID: 1449465
 TI Isolation and characterization of two **opioid** peptides from a **bovine hemoglobin** peptic hydrolysate.
 AU Piot J M; Zhao Q; Guillochon D; Ricart G; Thomas D
 CS Laboratoire de Technologie des Substances Naturelles, Villeneuve D'Ascq, France.
 SO BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1992 Nov 30) 189
 (1) 101-10.
 Journal code: 0372516. ISSN: 0006-291X.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 EM 199212
 ED Entered STN: 19930129
 Last Updated on STN: 19930129
 Entered Medline: 19921230
 AB Two **opioid** peptides were isolated from a **bovine hemoglobin** hydrolysate, by use of gel permeation (GP) and reverse phase (RP) high performance liquid chromatography (HPLC). Their primary structure and accurate molecular weights, determined by amino acid analysis and fast atom bombardment (FAB) mass spectrometry, were identical to fragments 31-40 (LVV-hemorphin-7) and 32-40 (VV-hemorphin 7) of the **beta-chain** of **bovine hemoglobin**. The same fragments occur in human hemoglobin in positions 32-41 and 33-41 of the **beta-chain**, respectively. The **opioid** potency of these peptides, exhibited by use of electrically stimulated muscle of isolated guinea-pig ileum (GPI), were significant and comparable with some others previously described. In addition, the location of the two **opioid** peptides, VV-hemorphin-7 and LVV-hemorphin-7, revealed the existence of a "strategic zone" both in the bovine and human **beta-chains** of hemoglobin.

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L2 ANSWER 3 OF 6 MEDLINE
 AN 95305417 MEDLINE
 DN 95305417 PubMed ID: 7785876
 TI Peptic hemoglobin hydrolysis in an ultrafiltration reactor at pilot plant scale generates **opioid** peptides.
 AU Zhao Q; Piot J M; Sannier F; Guillochon D
 CS Laboratoire de Genie Proteique, Faculte des Sciences de La Rochelle, France.
 SO ANNALS OF THE NEW YORK ACADEMY OF SCIENCES, (1995 Mar 31) 750 452-8. Journal code: 7506858. ISSN: 0077-8923.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 EM 199507
 ED Entered STN: 19950726
 Last Updated on STN: 19950726
 Entered Medline: 19950720
 AB Two hemorphins, peptides with **opioid** activity, have been isolated from a pepsin hydrolysate of **bovine hemoglobin**, by use of gel permeation (GP) and reverse phase (RP) high-performance liquid chromatography (HPLC). Their primary structure and accurate molecular weights, determined by amino acid analysis and fast atom bombardment (FAB) mass spectrometry, were identical to fragments 31-40 (LVV-hemorphin-7) and 32-40 (VV-hemorphin 7) of the **beta-chain of bovine hemoglobin**. Two other peptides, 34-40 (hemorphin-7) and 34-41 (hemorphin-8) of the **beta-chain of bovine hemoglobin**, have been synthesized and studied. The **opioid** potency of these peptides, exhibited by the use of electrically stimulated muscle of isolated guinea pig ileum (GPI), were significant and comparable with some others previously described. Studies of **opioid** activities and primary structure of hemorphins led us to postulate the important role of arginine and phenylalanine in **opioid** potency.

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L12 ANSWER 5 OF 105 MEDLINE
 AN 95341807 MEDLINE
 DN 95341807 PubMed ID: 7616689
 TI Effects of footshock-, psychological- and forced swimming-stress on the learning and memory processes: involvement of opioidergic pathways.
 AU Jodar L; Takahashi M; Kaneto H
 CS Department of Pharmacology, Faculty of Pharmaceutical Sciences, Nagasaki University, Japan.
 SO JAPANESE JOURNAL OF PHARMACOLOGY, (1995 Feb) 67 (2) 143-7.
 Journal code: 2983305R. ISSN: 0021-5198.
 CY Japan
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 EM 199508
 ED Entered STN: 19950905
 Last Updated on STN: 19950905
 Entered Medline: 19950824
 AB Modulation of learning and memory acquisition, retention and retrieval in the one trial passive avoidance learning task in mice by three inescapable stresses, i.e., footshock (FS), psychological (PSY) and forced swimming (SW) were investigated. Pre-, post-training and pre-test FS-stress (2 mA, 0.2 Hz, 1 sec for 30 min) and pre-training PSY-stress (communication box, 5 min) resulted in enhanced test latencies. On the contrary, SW-stress (20 degrees C, 5 min) immediately or 1 hr after training impaired retention latencies that tended to recover after 2 hr post-training SW-stress, suggesting that at least 2 hr are required to consolidate newly acquired information. In contrast, pre-stress **naloxone** (Nx), which did not affect FS- and PSY-stress induced facilitatory effects, returned to control levels the impaired retention latencies induced by SW-stress. Taken collectively, these results imply the involvement of an **opioid**-dependent mechanism in the modulation of **memory** by SW-stress and non-**opioid** in the case of FS- and PSY-stress. Furthermore, they suggest that different mechanisms are involved in stress-induced **memory** modifications and the production of stress-induced analgesia (SIA) since in the latter, FS and PSY but not SW stress produce Nx-sensitive antinociception.

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L12 ANSWER 7 OF 105 MEDLINE
 AN 95220477 MEDLINE
 DN 95220477 PubMed ID: 7705450
 TI Relationship between morphine and etonitazene-induced working memory impairment and analgesia.
 AU Braida D; Gori E; Sala M
 CS Institute of Pharmacology, Faculty of Mathematical, Physical and Natural Sciences, University of Milan, Italy.
 SO EUROPEAN JOURNAL OF PHARMACOLOGY, (1994 Dec 27) 271 (2-3) 497-504.
 Journal code: 1254354. ISSN: 0014-2999.
 CY Netherlands
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 EM 199505
 ED Entered STN: 19950518
 Last Updated on STN: 19950518
 Entered Medline: 19950509
 AB An 8-arm radial maze task was used to assess the possible role of the **opiate** system in the spatial **memory** of the rat. Increasing doses of etonitazene (0.005-0.06 mg/kg i.p.) and morphine (2.5-100 mg/kg i.p.) significantly impaired performance in the working memory components of the task. For both drugs this impairment was linearly related to the log of the administered dose, and the log-dose relationships were parallel. The regression lines calculated for each parameter for both drugs were parallel thus allowing us to calculate the potency: etonitazene proved to about 1000 times more potent than morphine in terms of correct arm entries, the number of errors and the total time taken to complete the task. Moreover, the progressive cognitive impairment produced by both opiates was closely related to an increase in analgesic effect. Pretreatment with **naloxone** (5 mg/kg i.p.) completely antagonised the disruptive effect of the **opiates** on working **memory**. The importance of the mu subtype **opiate** receptor in cognitive processes is discussed.

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L11 ANSWER 5 OF 215 MEDLINE
 AN 96145761 MEDLINE
 DN 96145761 PubMed ID: 8593578
 TI Brain sites involved in mu-opioid receptor-mediated actions: a 2-deoxyglucose study.
 AU Fabian I; Ableitner A
 CS Institute of Pharmacology, Toxicology and Pharmacy, Veterinary Faculty, University of Munich, Germany.
 SO BRAIN RESEARCH, (1995 Oct 30) 697 (1-2) 205-15.
 Journal code: 0045503. ISSN: 0006-8993.
 CY Netherlands
 DT Journal; Article; (JOURNAL ARTICLE).
 LA English
 FS Priority Journals
 EM 199604
 ED Entered STN: 19960422
 Last Updated on STN: 20000303
 Entered Medline: 19960411
 AB Brain regions that may be functionally involved in the neuropharmacological actions of mu-opioid agonists have been examined in conscious rats using the quantitative [¹⁴C]2-deoxyglucose autoradiographic technique. At 0.5 microgram and 1 microgram intracerebroventricularly the highly selective mu-opioid receptor agonist D-Ala2, MePhe4, Gly-ol5-enkephalin effected statistically significant increases as well as statistically significant decreases in regional glucose utilization: in limbic structures, such as hippocampal formation, medial amygdala and lateral septum, glucose utilization was most prominently increased after D-Ala2, MePhe4, Gly-ol5-enkephalin; glucose utilization was further increased in the lateral habenular nucleus, the hypothalamus, ventromedial nucleus and dorsal raphe; whereas decreases were found in the mamillary body and anterior thalamus. Glucose utilization in structures associated with somatosensory and nociceptive processing was increased in the central gray of the midbrain and decreased in the nucleus gelatinosus. Only increases in glucose utilization were produced by D-Ala2; MePhe4, Gly-ol5-enkephalin in brain regions involved in motor control, including the globus pallidus, the substantia nigra, pars reticulata, the nucleus ruber and the cerebellum, and brain regions involved in visual processing--the visual cortex and superior colliculus deep layer. It is concluded that this pattern of regional changes underlies the mu-opioid receptor-mediated antinociceptive-, epileptogenic-, memory- and mood-modulating actions of mu-opioid agonists.

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L12 ANSWER 10 OF 105 MEDLINE
 AN 95093656 MEDLINE
 DN 95093656 PubMed ID: 8000575
 TI **Naloxone** ameliorates the learning deficit induced by
 pentylenetetrazol kindling in rats.
 AU Becker A; Grecksch G; Brosz M
 CS Institute of Pharmacology and Toxicology, Faculty of Medicine,
 Otto-von-Guericke University Magdeburg, Germany.
 SO EUROPEAN JOURNAL OF NEUROSCIENCE, (1994 Sep 1) 6 (9) 1512-5.
 Journal code: 8918110. ISSN: 0953-816X.
 CY ENGLAND: United Kingdom
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 EM 199501
 ED Entered STN: 19950215
 Last Updated on STN: 19950215
 Entered Medline: 19950125
 AB Endogenous **opioid** peptides modulate and regulate processes of
 central excitability. Furthermore, **opioids** are thought to
 interfere with processes of **learning** and **memory**
 storage. In order to study the effects of endogenous **opioids** on
 both processes we injected in the course of development of
 pentylenetetrazol kindling the opiate receptor antagonist **naloxone**
 , and tested the animals afterwards in a shuttle-box task. It was found
 that **naloxone** pretreatment had dissociative effects. There was
 no effect on seizure outcome, whereas the **learning** deficit was
 ameliorated in the kindled group. The data suggest that endogenous
opioid peptides contribute to the **learning** deficit found
 in pentylenetetrazol-kindled rats.

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L12 ANSWER 1 OF 105 MEDLINE
 AN 96155020 MEDLINE
 DN 96155020 PubMed ID: 8587905
 TI **Memory** retrieval enhancement by kappa **opioid** agonist
 and mu, delta antagonists.
 AU Ilyutchenok R Y; Dubrovina N I
 CS Laboratory of the Memory Mechanisms, Institute of Physiology Siberian
 Branch of the Russian Academy of Medical Sciences, Novosibirsk, Russia.
 SO PHARMACOLOGY, BIOCHEMISTRY AND BEHAVIOR, (1995 Dec) 52 (4)
 683-7.
 Journal code: 0367050. ISSN: 0091-3057.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 EM 199603
 ED Entered STN: 19960404
 Last Updated on STN: 19960404
 Entered Medline: 19960327
 AB The present study sought to identify specific **opioid** receptor
 subtypes involved in the modulation of reactivation of amnesic or
 forgotten **memory** traces by use of a one-trial inhibitory
 avoidance training procedures in mice. The effects of **naloxone**,
 ICI 174,864 (mu and delta opioid receptor antagonists, respectively) and
 dynorphin (kappa agonist) were investigated. The results indicated that
 preretention test administration of **naloxone** (2 mg/kg) or ICI
 174,864 (3 mg/kg) attenuated the amnesia and forgetting as indicated by
 prolongation of step-through latency. On the other hand, the activation
 of kappa opioid receptors by dynorphin (1 mg/kg) also showed reactivating
 effects both after amnesia and forgetting. On the basis of the
 parallelism of the effects for mu and delta opioid receptor antagonists and kappa
 agonist, and on the finding that all three **opioids** demonstrated
 a different degree of reactivation of amnesic and forgotten **memory**
 traces, it was concluded that mu, delta, and kappa **opioid**
 receptors contribute to the modulation of amnesia and forgetting by
 independent mechanisms.

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L2 ANSWER 3 OF 3 MEDLINE
AN 94311913 MEDLINE
DN 94311913 PubMed ID: 8037741
TI Isolation of endogenous hemorphin-related hemoglobin fragments from bovine brain.
AU Karelin A A; Philippova M M; Karelina E V; Ivanov V T
CS Shemyakin and Ovchinnikov Institute of Bioorganic Chemistry, Russian Academy of Sciences, Moscow.
SO BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1994 Jul 15) 202 (1) 410-5.
Journal code: 0372516. ISSN: 0006-291X.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199408
ED Entered STN: 19940825
Last Updated on STN: 19940825
Entered Medline: 19940815
AB Six short-chain peptides were isolated from an acidic extract of bovine brain in the course of total peptide screening. Their primary structures determined by Edman degradation were ³¹⁻³⁵LVVYP, ³¹⁻³⁷LVVYPWT, ³¹⁻³⁸LVVYPWTQ, ³¹⁻³⁹LVVYPWTQRF, ³¹⁻⁴⁰VVYPWTQ and ³¹⁻⁴¹VVYPWTQRF, which respectively corresponded to the fragments 31-35, 31-37, 31-38, 31-40, 32-38 and 32-40 of bovine hemoglobin beta-chain. All these peptides contained sequences of opioid peptides - hemorphins. For two of these peptides, viz. 32-38 and 31-40, isolated from other sources, an opioid activity was demonstrated formerly.

opioid.
activity

in learning memory

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L6 ANSWER 73 OF 89 MEDLINE
 AN 89129128 MEDLINE
 DN 89129128 PubMed ID: 3222356
 TI Behavioral effects of **angiotensin** II and **angiotensin** II-(4-8)-pentapeptide in rats.
 AU Braszko J J; WLasienko J; Kupryszewski G; Witczuk B; Wisniewski K
 CS Department of Pharmacology, Medical Academy, Bialystok, Poland.
 SO PHYSIOLOGY AND BEHAVIOR, (1988) 44 (3) 327-32.
 Journal code: 0151504. ISSN: 0031-9384.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 EM 198903
 ED Entered STN: 19900308
 Last Updated on STN: 19970203
 Entered Medline: 19890323
 AB One nM of **angiotensin** II (AII) or **angiotensin** II-(4-8)-pentapeptide [AII(4-8)] given intracerebroventricularly did not affect locomotor and exploratory behavior of rats in open field. AII significantly increased and AII(4-8) did not affect vertical activity of animals in electromagnetic motimeter. Neither of the peptides influenced horizontal activity in the motimeter. Both peptides intensified stereotypy produced by apomorphine and amphetamine. AII significantly improved, while AII(4-8) did not affect, consolidation of **memory** of the correct way to food in T-maze. Similarly, AII increased and AII(4-8) did not change the rate of acquisition of conditioned avoidance responses in a shuttle-box. Of the two examined peptides only AII significantly improved retrieval of **memory** of the passive avoidance behavior. The results show that AII(4-8) influences central dopaminergic system but, unlike its parent peptide AII, has no apparent effect on **memory**.

L6 ANSWER 74 OF 89 MEDLINE
 AN 88335764 MEDLINE
 DN 88335764 PubMed ID: 3420007
 TI Effect of **angiotensin** II and saralasin on motor activity and the passive avoidance behavior of rats.
 AU Braszko J J; Wisniewski K
 CS Department of Pharmacology, Medical Academy, Bialystok, Poland.
 SO PEPTIDES, (1988 May-Jun) 9 (3) 475-9.
 Journal code: 8008690. ISSN: 0196-9781.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 EM 198810
 ED Entered STN: 19900308
 Last Updated on STN: 19970203
 Entered Medline: 19881021
 AB One nmole of **angiotensin** II (ANG II) or saralasin, given intracerebroventricularly, failed to alter the motor activity of rats in open field. A combined injection of both peptides caused a significant decrease of the number of crossings and rearings. In the electromagnetic motimeter horizontal activity of animals was changed by neither of the peptides while the vertical activity was increased by ANG II. Again, a combined injection of saralasin and ANG II inhibited both horizontal and vertical activity. Stereotypies evoked by both apomorphine (2 mg/kg) and

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amphetamine (6.5 mg/kg), given intraperitoneally, were markedly intensified by ANG II and saralasin. A five-fold increase of the re-entry latencies in the passive avoidance situation was observed after pre-test administration of ANG II or saralasin but not the two in combination. These results suggest that ANG II and saralasin may improve processes related to **learning** and **memory** through an unspecific mechanism involving central dopamine systems.

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L6 ANSWER 69 OF 89 MEDLINE
 AN 89295885 MEDLINE
 DN 89295885 PubMed ID: 3252173
 TI **Angiotensin** II-(3-8)-hexapeptide affects motor activity,
 performance of passive avoidance and a conditioned avoidance response in
 rats.
 AU Braszko J J; Kupryszewski G; Witczuk B; Wisniewski K
 CS Department of Pharmacology, Medical Academy, Bialystok, Poland.
 SO NEUROSCIENCE, (1988 Dec) 27 (3) 777-83.
 Journal code: 7605074. ISSN: 0306-4522.
 CY ENGLAND: United Kingdom
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 EM 198908
 ED Entered STN: 19900309
 Last Updated on STN: 19900309
 Entered Medline: 19890801
 AB **Angiotensin** II-(3-8)-hexapeptide, at the dose of 1 nmol given
 intracerebroventricularly, only slightly less than **angiotensin**
 II (the same dose and route) stimulated exploratory locomotor behaviour
 in
 an open field and electromagnetic motimeter. Both peptides considerably
 enhanced stereotyped behaviour produced by apomorphine and amphetamine.
Angiotensin II-(3-8)-hexapeptide improved recall in a passive
 avoidance situation as well as **angiotensin** II. The 3-8
 C-terminus of **angiotensin** II enhanced acquisition of active
 avoidance nearly as effectively as the complete peptide. The results
 indicate that the effectiveness of equimolar doses of **angiotensin**
 II-(3-8)-hexapeptide and **angiotensin** II in improving processes
 related to **learning** and **memory** in rats is almost
 identical and thus must be independent of specific **angiotensin**
 receptors in brain to which the hexapeptide binds with about 1000 times
 lower affinity than **angiotensin** II. The stimulation of
 stereotypy, a dopamine-controlled behaviour, by the peptides points to
 the
 possibility of dopaminergic mediation of their psychotropic effects.

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L6 ANSWER 51 OF 89 MEDLINE
 AN 94036192 MEDLINE
 DN 94036192 PubMed ID: 8221142
 TI **Angiotensin** II(3-8) (ANG IV) hippocampal binding: potential role
 in the facilitation of **memory**.
 AU Wright J W; Miller-Wing A V; Shaffer M J; Higginson C; Wright D E;
 Hanesworth J M; Harding J W
 CS Department of Psychology, Washington State University, Pullman
 99164-4820.
 NC HL-32063 (NHLBI)
 SO BRAIN RESEARCH BULLETIN, (1993) 32 (5) 497-502.
 Journal code: 7605818. ISSN: 0361-9230.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 EM 199312
 ED Entered STN: 19940117
 Last Updated on STN: 19940117
 Entered Medline: 19931207
 AB The present research characterizes a newly discovered ANG II(3-8) (ANG
 IV)
 binding site localized in structures associated with **memory**
 function (hippocampus, neocortex, cerebellum), as well as other brain
 stem
 structures (thalamus, inferior olivary nucleus). This site is not the AT1
 or AT2 site that binds **angiotensins** II (ANG II) and III (ANG
 III) nor does it bind the nonpeptide AT1 or AT2 receptor antagonists
 DuP753 and PD123177, respectively. The intracerebroventricular (ICV)
 infusion of ANG IV was ineffective at inducing drinking in rats as
 compared with equivalent doses of ANG II and III. Although not as
 effective as ANG II or ANG III, ICV infusion of ANG IV did provoke a
 pressor response at the highest dose (100 pmol/min), which appeared to be
 mediated by ANG II (AT1)-type receptors and not the specific AIV binding
 site described here. By contrast, the ICV infusion of ANG IV resulted in
 greater effects upon retention and retrieval of a passive avoidance task
 as compared with ANG II. Specifically, ANG II was not different from the
 ICV infusion of artificial cerebrospinal fluid, while ANG IV improved
 retention and retrieval of this task.

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L6 ANSWER 43 OF 89 MEDLINE
 AN 95400763 MEDLINE
 DN 95400763 PubMed ID: 7670888
 TI **Angiotensin** II and its 3-7 fragment improve recognition but not spatial **memory** in rats.
 AU Braszko J J; Kulakowska A; Wisniewski K
 CS Department of Pharmacology, Bialystok Medical Academy, Poland.
 SO BRAIN RESEARCH BULLETIN, (1995) 37 (6) 627-31.
 Journal code: 7605818. ISSN: 0361-9230.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 EM 199510
 ED Entered STN: 19951026
 Last Updated on STN: 19951026
 Entered Medline: 19951018
 AB The effects of **angiotensin** II (AII), its 3-7 fragment [AII(3-7)] and the substituted 3-7 fragment [Leu-5,AII(3-7)] given intracerebroventricularly (ICV) at the dose of 1 nmole each, on spatial **memory** and recognition were tested. AII(3-7) increased while Leu-5,AII(3-7) slightly decreased session to session foot shock reinforced runtime to the goal in a complex 6 chamber maze. The animals treated with AII performed in the maze similarly to saline injected controls. Overall number of errors was unchanged in all peptide treated groups in comparison. with the control group. Object recognition was significantly improved in all the peptide treated groups except for the Leu-5,AII(3-7) group. The results point to the facilitation of recognition and lack of influence on, or even attenuation of, spatial **memory** by AII and its 3-7 fragment. Leu-5,AII(3-7) caused similar though less pronounced effects.

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L6 ANSWER 41 OF 89 MEDLINE
 AN 96260253 MEDLINE
 DN 96260253 PubMed ID: 8787210
 TI The contribution of AT1 and AT2 **angiotensin** receptors to its cognitive effects.
 AU Braszko J
 CS Clinical Pharmacology Unit, Medical Academy of Bialystok, Poland.
 SO ACTA NEUROBIOLOGIAE EXPERIMENTALIS, (1996) 56 (1) 49-54.
 Journal code: 1246675. ISSN: 0065-1400.
 CY Poland
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 EM 199609
 ED Entered STN: 19961008
 Last Updated on STN: 19980206
 Entered Medline: 19960923
 AB In this study I attempted to assess, in rats, the role of AT1 and AT2 **angiotensin** receptor subtypes in the phenomenon of improved **learning** and **memory** after an intracerebroventricular (icv) injection of **angiotensin** II (Ang II) and Ang II (3-7). Selective AT1 (losartan, 1 mg) or AT2 (CGP 42112 A, 2 micrograms) receptor antagonist was dissolved in 2 microliters of saline and given to the left cerebral ventricle 5 min before 1 nmol Ang II or Ang II (3-7) injected in the same volume of saline to the right ventricle. Consequently, there were 9 experimental groups which underwent 3 **memory** oriented and 3 auxiliary tests. Ang II and Ang II (3-7) significantly improved retention of the passive avoidance and recognition **memory**. These effects were abolished by losartan or CGP 42112 A. Better, after Ang II and Ang II (3-7), acquisition of conditioned avoidance responses was unchanged by losartan and abolished by CGP 42112 A. None of the treatments significantly changed rats motor behaviour in open field. Losartan as well as CGP 42112 A abolished significant enhancement of apomorphine (1 mg/kg, i.p.) stereotypy caused by Ang II and Ang II (3-7). The results suggest considerable involvement of AT1 and AT2 **angiotensin** receptors in the cognitive enhancement produced by **angiotensins**.

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L6 ANSWER 75 OF 89 MEDLINE
 AN 88077383 MEDLINE
 DN 88077383 PubMed ID: 3689567
 TI Psychotropic effects of **angiotensin** II and III in rats:
 locomotor and exploratory vs cognitive behaviour.
 AU Braszko J J; Wisniewski K; Kupryszewski G; Witczuk B
 CS Department of Pharmacology, Medical Academy, Bialystok, Poland.
 SO BEHAVIOURAL BRAIN RESEARCH, (1987 Sep) 25 (3) 195-203.
 Journal code: 8004872. ISSN: 0166-4328.
 CY Netherlands
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 EM 198802
 ED Entered STN: 19900305
 Last Updated on STN: 19900305
 Entered Medline: 19880217
 AB One nmol of **angiotensin** II (AII) or **angiotensin** III
 (AIII) given intracerebroventricularly (i.c.v.) increased locomotor and
 exploratory activity in an open field apparatus but not in the
 electromagnetic field motimeter. Both peptides significantly enhanced
 stereotyped behaviour produced by apomorphine (2 mg/kg) and amphetamine
 (6.5 mg/kg) given intraperitoneally. Also, AII and AIII improved
 consolidation but not retrieval of **memory** for an appetitively
 reinforced spatial discrimination task in a T-maze. AII as well as AIII,
 given prior to the **learning** session on day 1, increased rate of
 acquisition of conditioned avoidance responses in a shuttle-box over the
 next 7 days. Both **angiotensins**, injected i.c.v. 15 min before
 the retention testing, remarkably (5-fold) prolonged re-entry latencies
 in the passive avoidance situation, suggesting facilitation of the retrieval
 of **memory** for an aversively motivated behaviour.

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